

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2003, 20:38:13 ; Search time 304 Seconds

(without alignments)
7511.600 Million cell updates/sec

Title: US-10-023-775b-1

Perfect score: 1014
Sequence: 1 atgaatgagccactagacta.....gttactcaaacaccttga 1014

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

N.Geneseq_101002:*

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- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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- 8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
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- 10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
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- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1014	100.0	1014	24	ABQ78847 Human G-protein co
2	1014	100.0	1014	24	AAD34278 Human AXOR89 (G-pr
3	1014	100.0	1014	24	AAD26370 Human G-protein co
4	1012.4	99.8	1014	22	AA507948 Human CDNA encodin
5	1012.4	99.8	1014	24	ABR85630 Human P2Y-like rec
6	1012.4	99.8	1014	24	ABR11381 Human DNA encoding
7	1012.4	99.8	1014	24	AAK98323 Human purinergic-r
8	1012.4	99.8	1288	24	ABL56197 Human P2Y1-1l enco
9	1012.4	99.8	5435	24	ABL56198 Human P2Y1-1l enco

10	1012.4	99.8	9905	24	AAK98324	Human purinergic-r
11	1010.8	99.7	1729	22	AA508362	Human CDNA encodin
12	1010.8	99.7	1729	23	ABY24026	Human prostate exp
13	1010.8	99.7	1729	23	ABY25767	Human prostate exp
14	1010.8	99.7	1729	23	ABY29909	Human prostate exp
15	1010.8	99.7	1729	23	ABY30024	Human prostate exp
16	1009.4	99.5	1011	24	AA43942	Human G-protein-co
17	976.2	96.3	1020	22	AA451011	Human ngPCR54 codi
18	829.4	81.8	831	24	ABN85629	Human P2Y-like rec
19	728	71.8	1313	22	AAK52430	Human polynucleoti
20	560.8	55.3	740	23	AAK51562	Human prostate exp
21	537.2	53.0	578	22	AAH50998	Human ngPCR54 codi
22	481.4	47.5	545	22	ABA08326	Human P2Y purinoc
23	481.4	47.5	545	22	AAK53414	Human polynucleoti
24	426.2	42.0	539	23	ABY39127	Human prostate exp
25	426.2	42.0	539	23	ABY4465	Human prostate exp
26	343.4	33.9	478	23	ABY15479	Human prostate exp
27	341.4	33.7	426	23	ABY36271	Human prostate exp
28	341.4	33.7	426	23	ABY45310	Human prostate exp
29	338.2	33.4	442	23	ABY08973	Human prostate exp
30	332	32.7	2245	24	ABK11380	Human P2Y1-like G
31	322	31.8	435	23	ABY06310	Human prostate exp
32	189	18.6	657	22	AA530831	Human CDNA encodin
33	149.4	14.7	6721	24	AA518600	Purinergic recepto
34	148.6	14.7	6721	24	AA518599	Purinergic recepto
35	136	13.4	1428	18	AA775146	Human ATP receptor
36	129.6	12.8	1005	21	AA011335	Human orphan G pro
37	129.6	12.8	1005	21	AAA46036	Human G-protein co
38	129.6	12.8	1436	24	ABL90790	Human polynucleoti
39	129.6	12.8	1542	24	AA24958	Human G-protein co
40	127.8	12.6	8423	24	ABL33407	Human immune syste
41	127.4	12.6	1385	21	AA081122	Human secreted pro
42	127.4	12.6	1996	18	AA771900	Human purinergic r
43	125	12.3	1543	24	ABK12937	DNA sequence of mo
44	121.4	12.0	1429	18	AA774321	Human P2Y4 recepto
45	108.2	10.7	1163	22	AA04981	Human purinergic r

ALIGNMENTS

RESULT 1	ABQ78847	standard; cDNA; 1014 BP.
ID	ABQ78847	
AC	ABQ78847	
DT	04-OCT-2002	(first entry)
XX	Human G-protein coupled receptor P2Y-019	CDNA.
DE	Human G-protein coupled receptor P2Y-019	CDNA.
KW	Human; G-protein coupled receptor; GPCR; P2Y-019; neuroprotective;	
KW	anti-inflammatory; cytosolic; cardiovascular; antiallergic; hypotensive;	
KW	antiartherosclerotic; osteopathic; hypertension; asthma;	
KW	atherosclerosis; gene; ss.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	1..1014
FT		/*tag- a
FT		/product- "P2Y-019"
XX	EP1219638-A2.	
XX	03-JUL-2002.	
PD	04-DEC-2001; 2001EP-0310136.	
PF	18-DEC-2000; 2000GB-0030854.	
PR	04-MAY-2001; 2001GB-0011031.	
XX	(PFI2) PFIZER LTD.	

PS Claim 2; Page 30; 37pp; English.
 XX The invention relates to an isolated AXOR89 polypeptide (G-protein
 CC coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide
 CC and polynucleotide encoding the polypeptide, is useful for identifying
 CC agonists and antagonists (or inhibitors) that are potentially useful in
 CC treating conditions associated with an AXOR89 imbalance, such as
 CC bacterial, fungal or protozoan infections, cancers, pain, asthma,
 CC Parkinson's disease, diabetes, obesity, anorexia, bulimia, acute heart
 CC failure, hypotension, hypertension, urinary retention, osteoporosis,
 CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign
 CC prostatic hypertrophy, migraine, vomiting, psychotic and neurological
 CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia,
 CC dyskinesias, such as Huntington's Disease or Gilles de la Tourette's
 CC syndrome. The polynucleotide sequence may also be used for chromosome
 CC localization or tissue expression studies. The AXOR89 is used as a
 CC vaccine or to produce fusion proteins. The present sequence is human
 CC AXOR89 cDNA.
 SQ Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Query Match 100.0%; Score 1014; DB 24; Length 1014;
 Best Local Similarity 100.0%; Pred. No. 7.1e-289;
 Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTATAGCAAAATGCTTGTGATTTCCCGATTTATGAGCTGCT 60
 DB 1 ATGATGAGCCACTAGACTATTATAGCAAAATGCTTGTGATTTCCCGATTTATGAGCTGCT 60
 QY 61 TTTGGAATTTGACATGATGAAAAATCCCATCAAGATGACACTACCTCCCTGTTATTTAT 120
 DB 61 TTTGGAATTTGACATGATGAAAAATCCCATCAAGATGACACTACCTCCCTGTTATTTAT 120
 QY 121 GGCAATTATCTTCTGCTGGGATTTCCAGGCATGAGTGTATATCCACTTACATTTTC 180
 DB 121 GGCAATTATCTTCTGCTGGGATTTCCAGGCATGAGTGTATATCCACTTACATTTTC 180
 QY 181 AAAATGAGACCTTGGAGAGAGACACATCATTTATGCTGTAACCTGGCCGACAGATCTG 240
 DB 181 AAAATGAGACCTTGGAGAGAGACACATCATTTATGCTGTAACCTGGCCGACAGATCTG 240
 QY 241 CTGTATCTGACAGCCCTCCCTTCTGTATCTACTATGATGCGAGTGGCGAAAACTGATC 300
 DB 241 CTGTATCTGACAGCCCTCCCTTCTGTATCTACTATGATGCGAGTGGCGAAAACTGATC 300
 QY 301 TTTGGAATTTGATGATGATTTATCCGCTTACCTTCCATTTCAACCTGTATAGCAGC 360
 DB 301 TTTGGAATTTGATGATGATTTATCCGCTTACCTTCCATTTCAACCTGTATAGCAGC 360
 QY 361 ATTCCTTTCCTACCTGTTTTCAGATGCTCCGCTACTGATGATCATTACCCCAATGAGC 420
 DB 361 ATTCCTTTCCTACCTGTTTTCAGATGCTCCGCTACTGATGATCATTACCCCAATGAGC 420
 QY 421 TGCCTTTTCATTCACAAAACTGATGAGTGTAGCCTGTGCTGTGTGATCATT 480
 DB 421 TGCCTTTTCATTCACAAAACTGATGAGTGTAGCCTGTGCTGTGTGATCATT 480
 QY 481 TCACGTGATGCTGTATTCCTGATGACCTTCTTGTATCATCAACCAAGAGACCAAGAGA 540
 DB 481 TCACGTGATGCTGTATTCCTGATGACCTTCTTGTATCATCAACCAAGAGACCAAGAGA 540
 QY 541 TCAGCTGTGCTGACCTGACCTGATGAGTGTAGCAATATATTAAGGTGATCAACCTGA 600
 DB 541 TCAGCTGTGCTGACCTGACCTGATGAGTGTAGCAATATATTAAGGTGATCAACCTGA 600
 QY 601 ATTTGACGTGCAACTACTTTCCTCCCTTGTGATAGTATGACACTTGTATACAGC 660
 DB 601 ATTTGACGTGCAACTACTTTCCTCCCTTGTGATAGTATGACACTTGTATACAGC 660
 QY 661 ATTTATCCACTCTGACCCATGAGTGTGACAACTGACAGCTGCTTAAGCAGAAACAGAGA 720
 DB 661 ATTTATCCACTCTGACCCATGAGTGTGACAACTGACAGCTGCTTAAGCAGAAACAGAGA 720

QY 721 AGGCTAACCATTCCTGCTACTCCTTGCATTTTACGATGTTTATACCTTCATATCTTG 780
 DB 721 AGGCTAACCATTCCTGCTACTCCTTGCATTTTACGATGTTTATACCTTCATATCTTG 780
 QY 781 AGGCTATTCGATGCAATTCGCTGCTTTCATCATGTTTTCATGAGATGAGATC 840
 DB 781 AGGCTATTCGATGCAATTCGCTGCTTTCATCATGTTTTCATGAGATGAGATC 840
 QY 841 CATGAGCTTACATGCTTCTGATGACATTAAGCTGCTTCAACCTTTGGTATCCGTGA 900
 DB 841 CATGAGCTTACATGCTTCTGATGACATTAAGCTGCTTCAACCTTTGGTATCCGTGA 900
 QY 901 CTATATGCTGTGCTGACGACCAACTTTCAGACAGCTGTCTGCTCAACAGTATGCAAA 960
 DB 901 CTATATGCTGTGCTGACGACCAACTTTCAGACAGCTGTCTGCTCAACAGTATGCAAA 960
 QY 961 GTTAGCGGAGACCTTGACGACCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014
 DB 961 GTTAGCGGAGACCTTGACGACCAAGAAATTTAGTTACTCAAAACACCTTTGA 1014

RESULT 3
 AAD26370
 ID AAD26370 standard; cDNA; 1014 BP.
 XX
 AC AAD26370;
 DT 26-MAR-2002 (first entry)
 DE Human G-protein coupled receptor 2 (GCR2-2) cDNA.
 XX
 KW Human: G-protein coupled receptor 2; cell proliferative disorder;
 KW arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
 KW gastroduodenal disorder; dysphagia; anorexia; autoimmune disorder;
 KW acquired immune deficiency syndrome; inflammatory disorder; infection;
 KW Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;
 KW diabetes; obesity; osteoporosis; gene therapy; GCR2-2; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS 1..1014
 FT /tag= a
 FT /product= "human GCR2-2 protein"

WO200187937-A2.
 PD 22-NOV-2001.
 PE 17-MAY-2001; 2001WO-US16285.
 XX
 PR 18-MAY-2000; 2000US-205628P.
 PR 22-MAY-2000; 2000US-206222P.
 PR 25-MAY-2000; 2000US-207566P.
 PR 02-JUN-2000; 2000US-208834P.
 PR 02-JUN-2000; 2000US-208861P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 PI Patterson C, Lu DM, Thornton M, Lu Y, Tribouley CM, Graul R;
 PI Khan FA, Gandhi AR, Walla NK, Nguyen DB, Yue H, Hafalia A;
 PI Elliott VS, Lai P, Reddy R, Kallick DA, Tang TV, Au-Young J;
 XX
 DR WPI: 2002-089844/12.
 XX P-PSDB: AAE16171.
 PT Novel G-protein coupled receptors and polynucleotides useful for
 PT diagnosis, treatment and prevention of disorders of cell proliferation,
 PT neurological, cardiovascular, metabolic disorders and viral infections
 XX

PS Claim 5; Page 111-112; 115pp; English.

CC The invention relates to human G-protein coupled receptor (GPCR)
CC polypeptides and polynucleotides. GPCR polypeptides are useful for
CC screening compounds that modulate their activity. They are useful in
CC the diagnosis, prevention and treatment of disorders which include
CC cell proliferative disorders such as arteriosclerosis, hepatitis,
CC myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia
CC lymphoma, neurological disorders such as epilepsy, ischaemic
CC cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
CC Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral
CC meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia
CC cardiovascular disorders such as arteriovenous fistula, atherosclerosis
CC hypertension, vascular tumours, myocardial infarction, hypertensive
CC heart disease, infective endocarditis, cardiomyopathy, myocarditis;
CC gastrointestinal disorders such as dysphagia, peptic oesophagitis;
CC emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
CC constipation, acquired immune deficiency syndrome (AIDS), hepatic
CC encephalopathy; autoimmune/inflammatory disorders such as Addison's
CC disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact
CC dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,
CC emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid
CC arthritis, systemic lupus erythematosus, warts, viral, bacterial,
CC fungal, parasitic, protozoal and helminthic infections and trauma;
CC metabolic disorders such as diabetes, obesity and osteoporosis; and
CC viral infections such as infection caused by viral agent classified as
CC adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention
CC are useful as probes for assessing toxicity of test compounds. They are
CC also used in gene therapy. The present sequence is human G-protein
CC coupled receptor 2 (GCR2-2) cDNA.

SQ Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Query Match	100.0%	Score 1014:	DB 24:	Length 1014:
Best Local Similarity	100.0%:	Pred. No. 7.1e+289:		
Matches 1014, Conservative	0:	Mismatches 0:	Indels 0:	Gaps 0

QY	1	ATGATATGAGCCACTAGACATATTAGCAATGCTTCGATTTTCCCAGATTATGACAGCTGCT	60
Db	1	ATGATATGAGCCACTAGACATATTAGCAATGCTTCGATTTTCCCAGATTATGACAGCTGCT	60
QY	61	TTTGGAAATTTGCATGATGAAAAACAATCCACATCCAGATGACACTACCTCCCTGTTATTTAT	120
Db	61	TTTGGAAATTTGCATGATGAAAAACAATCCACATCCAGATGACACTACCTCCCTGTTATTTAT	120
QY	121	GGCATTATCTTCCTCGTGGGATTTTCCAGGCAATGCAATGAGTAGTATATCCATTACATTTTC	180
Db	121	GGCATTATCTTCCTCGTGGGATTTTCCAGGCAATGCAATGAGTAGTATATCCATTACATTTTC	180
QY	181	AAATATGAGACCTTGGANAGACAGACACATCATTTATGCTGAACCTGGCCTGCACAGATCTG	240
Db	181	AAATATGAGACCTTGGANAGACAGACACATCATTTATGCTGAACCTGGCCTGCACAGATCTG	240
QY	241	CTGTATTCGACCAAGCCTCCCTTCCTCGATTCACTACTATTATGCCAGTGGGAAAACTGGATC	300
Db	241	CTGTATTCGACCAAGCCTCCCTTCCTCGATTCACTACTATTATGCCAGTGGGAAAACTGGATC	300
QY	301	TTTGAGAGATTTCAATGTTATTTATATCCGCTTCAGCTTCATTCATTAACCGTATATAGAGC	360
Db	301	TTTGAGAGATTTCAATGTTATTTATATCCGCTTCAGCTTCATTCATTCATTAACCGTATATAGAGC	360
QY	361	ATCCTCTTCCTACACCTGTTTCAGACATCTTCCGCTACTGTTGTATTCATTCACCCAAATGAGC	420
Db	361	ATCCTCTTCCTACACCTGTTTCAGACATCTTCCGCTACTGTTGTATTCATTCACCCAAATGAGC	420
QY	421	TGCTTTTCATTCACAAAACTCGATGTGCAATTTAGCCTGTGCTGTGCTGTGGATTCATT	480
Db	421	TGCTTTTCATTCACAAAACTCGATGTGCAATTTAGCCTGTGCTGTGCTGTGGATTCATT	480
QY	481	TCACATGGATGCTGATATTCGCAATGACCTCTTGATACATCAACCAACAGACCAACAGAGA	540
Db	481	TCACATGGATGCTGATATTCGCAATGACCTCTTGATACATCAACCAACAGACCAACAGAGA	540

OY	541	TCAGCCGTCGTGACCTGCACAGTTGGGATGGAATGACATATTAATGGTACACCTTA	6000
Db	541	TCAGCCGTCGTGACCTGCACAGTTGGGATGGAATGACATATTAATGGTACACCTTA	6000
OY	601	ATTATTGACATGCACATCTTTCTGCGTCCCTTGGTATAGTACACTTTGCTATACGACG	6600
Db	601	ATTATTGACATGCACATCTTTCTGCGTCCCTTGGTATAGTACACTTTGCTATACGACG	6600
OY	661	ATTATTCACACTGTGACCCATGAGACTGCGAAACTGACAGCTGCTTAAGCAGAAAGCAGA	7200
Db	661	ATTATTCACACTGTGACCCATGAGACTGCGAAACTGACAGCTGCTTAAGCAGAAAGCAGA	7200
OY	721	AGGCTAACCACTTGTGCTACTCCCTTGCATTTTACGATGTGTTTTTACCTTCATATCTTG	7800
Db	721	AGGCTAACCACTTGTGCTACTCCCTTGCATTTTACGATGTGTTTTTACCTTCATATCTTG	7800
OY	781	AGGCTCACTTCGATGCAATCTGCGCTGCTTCAATCAGTTGCTCCATTGAGATCAGATC	8400
Db	781	AGGCTCACTTCGATGCAATCTGCGCTGCTTCAATCAGTTGCTCCATTGAGATCAGATC	8400
OY	901	CTATATGTGGTGGTACGACGACAATTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAA	9600
Db	901	CTATATGTGGTGGTACGACGACAATTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAA	9600
OY	961	GTAAGCGGGAACCTTGAGCAGCAAGAAAGAAATTAATTACTCTCAACACACCTTTGA	1014
Db	961	GTAAGCGGGAACCTTGAGCAGCAAGAAAGAAATTAATTACTCTCAACACACCTTTGA	1014
RESULT 4			
AA507948	AA507948 standard; cDNA; 1014 bp.		
ID	AA507948		
XX	AA507948;		
AC	23-OCT-2001 (first entry)		
XX	Human cDNA encoding G-protein coupled receptor, hrUP21.		
DT	Human; G-protein coupled receptor; GPCR; hrUP21; agonist;		
XX	Inverse agonist; lung cancer; ss.		
KM	Homo sapiens.		
XX	Key		
FT	Location/Qualifiers		
FT	1..1014		
FT	/*tag= a		
FT	/product= "hrUP21"		
PN	WO200136471-A2.		
XX	25-MAY-2001.		
PD	16-NOV-2000; 2000MO-US31509.		
XX	17-NOV-1999; 99US-0166088.		
PR	17-NOV-1999; 99US-0166099.		
PR	17-NOV-1999; 99US-0166369.		
PR	23-DEC-1999; 99US-0171900.		
PR	23-DEC-1999; 99US-0171901.		
PR	23-DEC-1999; 99US-0171902.		
PR	11-FEB-2000; 2000US-0181749.		
PR	14-MAR-2000; 2000US-0189258.		
PR	14-MAR-2000; 2000US-0189259.		
PR	10-APR-2000; 2000US-0195889.		
PR	10-APR-2000; 2000US-0196078.		
PR	28-APR-2000; 2000US-0200419.		
PR	12-MAY-2000; 2000US-0203630.		

PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.
 XX
 PA (AREN-) ARENA PHARM INC.
 PI Chen R, Dang HT, Lowitz KP;
 XX
 DR WPI; 2001-355616/37.
 DR P-PSDB; AAU04375.
 XX
 PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -
 XX
 PS Claim 55, Page 113-114; 159pp; English.
 XX
 CC The sequence encodes a human G-protein coupled receptor (GPCR),
 CC hGPR1. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilized to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.
 XX
 SO Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 99.8%; Score 1012.4; DB 22; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 2.1e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTATACATTTTATGCAAAATGCTTCTGATTTCCCGCATTTATGACGCTGCT 60
 DB 1 ATGAATGAGCCACTATACATTTTATGCAAAATGCTTCTGATTTCCCGCATTTATGACGCTGCT 60
 QY 61 TTGGAATTTGCACTGATGATAAATCCCACTCAAGATGACATACCTCCCTGTTATTTAT 120
 DB 61 TTGGAATTTGCACTGATGATAAATCCCACTCAAGATGACATACCTCCCTGTTATTTAT 120
 QY 121 GGCATTATCTCTCTGCTGGGATTTCCAGGCAATGAGTAGATGATTCACATTTTC 180
 DB 121 GGCATTATCTCTCTGCTGGGATTTCCAGGCAATGAGTAGATGATTCACATTTTC 180
 QY 181 AAAATGAGACCTTGGGAAGGACACACATCATATATGCTGACCTGGCCTGCAAGATCTG 240
 DB 181 AAAATGAGACCTTGGGAAGGACACACATCATATATGCTGACCTGGCCTGCAAGATCTG 240
 QY 241 CTGTATCTGACAGCCTCCCTCTCTGATTTCACTATATGCGAGTGGCGAAATCTGATC 300
 DB 241 CTGTATCTGACAGCCTCCCTCTCTGATTTCACTATATGCGAGTGGCGAAATCTGATC 300
 QY 301 TTTGGAGATTTCAATGTGTAAGTTATTCGCGCTTCACTTCAACCTGTATATGACAGC 360
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 DB 481 TCACCTGTAGCTGTATTCGATGACCTTCTTGATCATATCAACCAAGAGACCAACAGA 540

QY 541 TCAGCCTGTCTCGACCTCACACAGTTCGATGATGAACTCAATATTAAGTGTACAACTTA 600
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 QY 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 961 GTAAGCGGGAACCTTGGAGCAAGCAAAATTAAGTATCTCAACCAACCTTGA 1014
 DB 961 GTAAGCGGGAACCTTGGAGCAAGCAAAATTAAGTATCTCAACCAACCTTGA 1014

RESULT 5
 ABN85630
 ID ABN85630 standard; DNA; 1014 BP.

AC ABN85630;
 XX
 AC 18-SEP-2002 (first entry)
 XX
 DE Human P2Y-1-like receptor variant encoding gene SEQ ID NO 3.
 XX
 KW Human; P2Y-1-like receptor; HIRPDM 0000037; immunity; inflammation;
 KW cancer; Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;
 KW immunomodulator; anti-inflammatory; cytostatic; antiallergic;
 KW gastrointestinal; anti-ulcer; antihypertensive; antidiabetic; antineoplastic;
 KW antibacterial; immunosuppressive; dermatological; nephrotoxic;
 KW antiallergic; analgesic; receptor; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1014
 FT /*tag- a
 FT /product- "P2Y-1-like receptor variant"
 XX
 PN GB2369364-A.
 PD 29-MAY-2002.
 XX
 PF 31-AUG-2001; 2001GB-0021215.
 XX
 PR 01-SEP-2000; 2000GB-0021524.
 PR 06-SEP-2000; 2000GB-0021894.
 PR 25-SEP-2000; 2000GB-0023444.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Record SM; Ignat DM;
 XX
 WPI; 2002-511268/55.

DR P-PSDB: ABB83819.

PT An isolated P2Y₁-like receptor polypeptide (HIPDM 0000037) which can be used for the identification of agonists and antagonists which may be used to treat an immune or inflammatory disease.

PS Claim 5; Page 28-29; 35pp; English.

CC The invention relates to an isolated P2Y₁-like receptor polypeptide (ABB83819-ABB83819) which is also referred to in the specification as HIPDM 0000037. An effective amount of a substance (agonist or antagonist) which modulates P2Y₁ receptor activity is useful to treat a subject having a disorder that is responsive to P2Y₁-like receptor modulation. The disorder is a disease of immunity or inflammation. The substance may also be used to manufacture a medicine for the treatment or prophylaxis of a disorder that is responsive to stimulation or modulation of P2Y₁-like receptor activity. Disorders which may be treated include colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome, gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative colitis, rheumatoid arthritis, viral diseases, bacterial infections, autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic rhinitis, inflammatory pain and general inflammation such as tendonitis, polymyositis or prostatitis. The invention provides alternative substances for the treatment of immunological and inflammatory diseases. The present sequence is that the P2Y₁-like receptor variant encoding gene of the invention.

SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 99.88; Score 1012.4; DB 24; Length 1014;

Best Local Similarity 99.98; Pred. No. 2.1e-288; Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGATATTTAGCAAAATGCTTGTATCCCGATTATGACAGTCT 60
 DB 1 ATGAATGAGCCACTAGATATTTAGCAAAATGCTTGTATCCCGATTATGACAGTCT 60
 QY 61 TTGGAAATTTGACATGATGAAATATCCCAATGATGACATGCTTGTATTTAT 120
 DB 61 TTGGAAATTTGACATGATGAAATATCCCAATGATGACATGCTTGTATTTAT 120
 QY 121 GGCAATTTTCCCGGAGGATTTCCAGCAATGACATGATGATGATGATGATGATGAT 180
 DB 121 GGCAATTTTCCCGGAGGATTTCCAGCAATGACATGATGATGATGATGATGATGAT 180
 QY 181 AAATGAGACCTTGGAGAGCAGACATCATTTATGCTGAACCTGGCTGCAGATCTG 240
 DB 181 AAATGAGACCTTGGAGAGCAGACATCATTTATGCTGAACCTGGCTGCAGATCTG 240
 QY 241 CTGTATCTGACACAGCTCCCTTCCTGATTCATGATGATGATGATGATGATGATGAT 300
 DB 241 CTGTATCTGACACAGCTCCCTTCCTGATTCATGATGATGATGATGATGATGATGAT 300
 QY 301 TTGGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 DB 301 TTGGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 QY 361 ATCCCTTCTCAGCTTTCAGATCTCCGCTGATGATGATGATGATGATGATGATGAT 420
 DB 361 ATCCCTTCTCAGCTTTCAGATCTCCGCTGATGATGATGATGATGATGATGATGAT 420
 QY 421 TGGTTTTCATGACAAATCGATGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 421 TGGTTTTCATGACAAATCGATGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 DB 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 541 TCAGCCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 541 TCAGCCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600

QY 601 ATTTTGAAGCACTACTTCTGCTCCCTGGTGTATGATGACACTTTGCTATACACG 660
 DB 601 ATTTTGAAGCACTACTTCTGCTCCCTGGTGTATGATGACACTTTGCTATACACG 660
 QY 661 ATTTTGAAGCACTACTTCTGCTCCCTGGTGTATGATGACACTTTGCTATACACG 720
 DB 661 ATTTTGAAGCACTACTTCTGCTCCCTGGTGTATGATGACACTTTGCTATACACG 720
 QY 721 AGGCTAACATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 721 AGGCTAACATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 QY 781 AGGCTAACATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 781 AGGCTAACATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 841 CATGACCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 841 CATGACCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 901 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 DB 901 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 QY 961 GTAAAGCGGAACTTGGAGCAAGCAAGAAATTAATGATGATGATGATGATGATGAT 1014
 DB 961 GTAAAGCGGAACTTGGAGCAAGCAAGAAATTAATGATGATGATGATGATGATGAT 1014

RESULT 6
 ABR11381
 ID ABR11381 standard; DNA; 1014 BP.

ABR11381;
 05-JUN-2002 (first entry)

Human DNA encoding P2Y₁-like G protein-coupled receptor.

Human; ds; gene; P2Y₁-like G protein-coupled receptor; GPCR;
 infection; pain; cancer; anorexia; bulimia; asthma; hypertension;
 central nervous system disease; acute heart failure; hypertension;
 urinary retention; osteoporosis; diabetes; angina pectoris;
 myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis;
 benign prostatic hyperplasia; psychosis; neurological disorder;
 dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder;
 Parkinson's disease; anxiety; schizophrenia; manic depression; delirium;
 dementia; severe mental retardation; Huntington's disease;
 Tourette's syndrome.

Homo sapiens.

Key Location/Qualifiers
 CDS 1..1014
 /tag= a
 /product= "P2Y₁-like GPCR"

W0200214511-A2.

21-FEB-2002.

10-AUG-2001; 2001WO-EP09243.

14-AUG-2000; 2000US-224989P.

(FARB) BAYER AG.

Ramakrishnan S;

WPI: 2002-257607/30.

P-PSDB: AAU77600.

Novel human P2Y₁-like G protein-coupled receptor polypeptide which can

PT be regulated for treating infection, pain, cancer, diabetes, anorexia,
 PT asthma, hypertension, neurological disorder and dyskinesia
 XX
 PS Claim 1, Fig 5, 118pp: English.

XX
 CC The invention relates to a purified human P2Y₁-like G protein-coupled
 CC receptor (GPCR) polypeptide and the nucleic acids encoding it
 CC (including 5' and 3' sequences, promoters, fragments, variants, or a
 CC sequence encoding a protein at least 50% identical to the GPCR).
 CC Also included are an expression vector comprising the nucleic acid,
 CC a host cell containing the vector and the identification of modulators of
 CC the GPCR especially those that reduce the activity of the GPCR.
 CC The nucleic acid is useful for detecting a polynucleotide encoding
 CC the GPCR in a biological sample. The GPCR and nucleic acid are useful for
 CC screening for agents which decrease the activity of the GPCR and
 CC for modulators of the GPCR. The modulator or agent useful for modulating
 CC the activity of P2Y₁-like G protein-coupled receptor in a disease such as
 CC bacterial, fungal, protozoan, and viral infection, pain, cancer,
 CC anorexia, bulimia, asthma, central nervous system (CNS) disease, acute
 CC heart failure, hypotension, hypertension, urinary retention,
 CC osteoporosis, diabetes, angina pectoris, myocardial infarction, ulcer,
 CC inflammation, allergy, multiple sclerosis, benign prostatic hypertrophy,
 CC psychotic and neurological disorders, dyskinesias, HIV virus infection
 CC (human immunodeficiency virus), CNS disorders such as Parkinson's
 CC disease, anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation, Huntington's disease and Tourette's syndrome.
 CC The present sequence encodes the P2Y₁-like GPCR of the invention.

XX
 SQ Sequence 1014 BP, 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 99.8%; Score 1012.4; DB 24; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 2,1e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTGACTATTATAGCAATGCTTCTGATTTCCCGATATGACGCTGCT 60
 DB 1 ATGAATGAGCCACTGACTATTATAGCAATGCTTCTGATTTCCCGATATGACGCTGCT 60
 QY 61 TTGGAAATGACGATGATAAATCCACATGAGATGACGATGCTGCTGCTGCTGCTGCT 120
 DB 61 TTGGAAATGACGATGATAAATCCACATGAGATGACGATGCTGCTGCTGCTGCTGCT 120
 QY 121 GGCATTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 121 GGCATTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 QY 181 AAAATGAGACCTTGGAGAGAGACACATCATTTATGCTGACCTGGCTGACAGATCTG 240
 DB 181 AAAATGAGACCTTGGAGAGAGACACATCATTTATGCTGACCTGGCTGACAGATCTG 240
 QY 241 CTGTATCTGACGAGCTCCCTCTGATTCCTACTGATGCTGATGCTGCTGCTGCTGCTGCT 300
 DB 241 CTGTATCTGACGAGCTCCCTCTGATTCCTACTGATGCTGATGCTGCTGCTGCTGCTGCT 300
 QY 301 TTGGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
 DB 301 TTGGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
 QY 361 ATCT 420
 DB 361 ATCT 420
 QY 421 TGCCTTTCATTCACAAAATCGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 480
 DB 421 TGCCTTTCATTCACAAAATCGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 480
 QY 481 TCACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 540
 DB 481 TCACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 540
 QY 541 TCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 DB 541 TCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

QY 601 ATTGAGTGCACACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 DB 601 ATTGAGTGCACACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 661 ATTATCCACTCTGACCCATGAGCTGACAACTGACAGCTGCTTATAGCAAGAAACGCA 720
 DB 661 ATTATCCACTCTGACCCATGAGCTGACAACTGACAGCTGCTTATAGCAAGAAACGCA 720
 QY 721 AGGCTACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 DB 721 AGGCTACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 781 AGGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 DB 781 AGGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 QY 841 CATGAAGCTTACATCTTCTGACCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 DB 841 CATGAAGCTTACATCTTCTGACCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 QY 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 DB 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 961 GTAAGGGGAGACCTGAGCAGCAAGAAATAGTACTCAAAACACCTTGA 1014
 DB 961 GTAAGGGGAGACCTGAGCAGCAAGAAATAGTACTCAAAACACCTTGA 1014

RESULT 7
 AAK98323
 ID AAK98323 standard; cDNA; 1014 BP.

XX AAK98323;
 XX 30-APR-2002 (first entry)

DE Human purinergic-related G-protein coupled receptor (GPCR) cDNA sequence.

KW Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;
 KW signal transduction; human protease; GPCR disorder; gene therapy;

KW transgenic animal; gene; ss.

OS Homo sapiens.

FX Key Location/Qualifiers

FT CDS 1..1014

FT FT /tag="a

FT FT /product="G-protein coupled receptor"

PN WO200187980-A2.

PN 22-NOV-2001.

PE 17-MAY-2001; 2001MO-US15957.

PR 18-MAY-2000; 2000US-205196P.

PR 08-AUG-2000; 2000US-0634656.

XX (APPL-) APPLERA CORP.

PI Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;

DR WPI; 2002-075312/10.

XX P-PSDB; AAO14027.

PT Novel isolated G-protein coupled receptor peptide useful for treating
 PT disorder characterised by absence of, in appropriate or unwanted
 PT expression of the receptor protein, and as immunogens to raise
 PT antibodies

PS Claim 23; Fig 1; 64pp; English.

XX The present specifically claimed human cDNA sequence (located on
 CC chromosome 13) encodes a purinergic-related G-protein coupled receptor
 CC (GPCR) of the invention. GPCRs constitute a major class of proteins
 CC responsible for signal transduction within a cell. Upon binding of a
 CC ligand to the extracellular portion of a GPCR, a signal is transduced
 CC resulting in a biological or physiological change within the cell. The
 CC GPCR proteins can be divided into five families, family I contains the
 CC purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are
 CC characterised by their selective responsiveness towards ATP and its
 CC analogues, some also respond to UTP. The invention comprises a human
 CC G-protein coupled receptor protein and encoding nucleic acids. The GPCR
 CC protein and nucleic acids of the invention are useful in the treatment of
 CC a disease or condition mediated by a human protease. The GPCR protein of
 CC the invention is useful for: the development/identification of
 CC therapeutic proteins; assays designed to quantitatively determine levels
 CC of the protein in biological fluids; identifying compounds which modulate
 CC the activity of the GPCR, or the interaction of the GPCR and a molecule
 CC with which it normally interacts; and treating a disorder characterised
 CC by an absence of, or inappropriate expression of the GPCR protein. The
 CC GPCR nucleic acids of the invention are useful in diagnostic assays to
 CC identify changes in the GPCR nucleic acid that lead to pathology;
 CC controlling GPCR expression; and in gene therapy to treat patients with
 CC aberrant GPCR gene expression. The GPCR nucleic acids can also be used in
 CC the production of transgenic animals.
 XX
 SX Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 99.8%; Score 1012.4; DR 24; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 2,1e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAGCCACTAGACTATTTAGCAAAATGCTTGTATTCGCCGATTAAGCAGTCT 60
 DB 1 ATGATGAGCCACTAGACTATTTAGCAAAATGCTTGTATTCGCCGATTAAGCAGTCT 60
 QY 61 TTTGGAATTTGCACTGATGAAACATCCACTCAAGATGCACTACCTCTGTTATTTAT 120
 DB 61 TTTGGAATTTGCACTGATGAAACATCCACTCAAGATGCACTACCTCTGTTATTTAT 120
 QY 121 GGCATTATCTTCCTCGGAGATTTCCAGCAATGCAATGCAATGCAATGCAATGCAAT 180
 DB 121 GGCATTATCTTCCTCGGAGATTTCCAGCAATGCAATGCAATGCAATGCAATGCAAT 180
 QY 181 AAATGAGACCTTGAAGAGACAGACCATTAATGCTGAACCTGCGCTCAGACAGATCTG 240
 DB 181 AAATGAGACCTTGAAGAGACAGACCATTAATGCTGAACCTGCGCTCAGACAGATCTG 240
 QY 241 CTGTATCTGACACAGCTCCCTCTCTGATTCATCTACTATGCGCAAGTGGCAAACTGATC 300
 DB 241 CTGTATCTGACACAGCTCCCTCTCTGATTCATCTACTATGCGCAAGTGGCAAACTGATC 300
 QY 301 TTTGGAATTTGCACTGATGAAACATCCACTCAAGATGCACTACCTCTGTTATTTAT 360
 DB 301 TTTGGAATTTGCACTGATGAAACATCCACTCAAGATGCACTACCTCTGTTATTTAT 360
 QY 361 ATCCCTTCCCTCACTGCTTCAAGATCTCCGCTACTGCTGATGATCAATCAACCAATGAGC 420
 DB 361 ATCCCTTCCCTCACTGCTTCAAGATCTCCGCTACTGCTGATGATCAATCAACCAATGAGC 420
 QY 421 TGCCTTTCCATTCACAAAACCTCGATGTCAGTTGTACCTGCTGCTGCTGCTGATCAT 480
 DB 421 TGCCTTTCCATTCACAAAACCTCGATGTCAGTTGTACCTGCTGCTGCTGCTGATCAT 480
 QY 481 TCACGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 DB 481 TCACGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 QY 541 TCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 DB 541 TCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
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DB 601 ATTTGACTGCAACTACTTTCCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 661 ATTTGACTGCAACTACTTTCCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 DB 661 ATTTGACTGCAACTACTTTCCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 QY 721 AGGTTACCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 DB 721 AGGTTACCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 781 AGGTTACCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 DB 781 AGGTTACCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 841 CATGACCTTACATGCTTTCAGACATTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 DB 841 CATGACCTTACATGCTTTCAGACATTTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 QY 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 DB 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 961 GTAAAGCGGAACTTGAAGCAAGCAAAATTAATGTTACTGCAAAACCACTTGA 1014
 DB 961 GTAAAGCGGAACTTGAAGCAAGCAAAATTAATGTTACTGCAAAACCACTTGA 1014

RESULT 8
 ABL56197
 ID ABL56197 standard; cDNA; 1288 BP.
 XX
 AC ABL56197;
 XX
 DE 05-JUL-2002 (first entry)
 XX
 DE Human P2Y1-11 encoding cDNA.
 XX
 KW Human; P2Y1-11; chromosome 13; G protein-coupled; receptor;
 KW gene therapy; thyroid; gene; ss.
 FT
 FT Homo sapiens.
 PN
 PN DE1046970-A1.
 PD 11-APR-2002.
 PF 22-SEP-2000; 2000DE-1046970.
 PF 22-SEP-2000; 2000DE-1046970.
 PR 22-SEP-2000; 2000DE-1046970.
 PR
 PA (BRUE/) BRUESS M.
 PA (BOEN/) BOENISCH H.
 XX
 PI Brues M, Boenisch H;
 XX
 DR WPI: 2002-35329/39.
 DR P-PSDB; ABB79438.
 XX
 PT New human P2Y111 gene, useful for treatment and diagnosis of associated
 PT diseases, and related proteins, antibodies and modulators, encodes G
 PT protein-coupled receptor
 XX
 PS Claim 5; Page 3; 5pp; German.
 XX
 CC The invention relates to the human P2Y111 gene (1), including its 5' and
 CC 3' untranslated regions, located on chromosome 13 and encoding a G
 CC protein-coupled receptor. (1) and related mRNA, cDNA, protein, antibodies

CC etc., are used for diagnosis and (gene) therapy of diseases that are
 CC (indirectly associated with (I) or its expression products. No diseases
 CC are specified but as (I) is expressed only in thyroid tissue, (I) is
 CC presumed to be involved in regulation of thyroid function. The present
 CC sequence is that of the P2Y11 encoding cDNA.

XX Sequence 1288 BP; 347 A; 318 C; 241 G; 382 T; 0 other;

Query Match 99.8%; Score 1012.4; DB 24; Length 1288;
 Best Local Similarity 99.9%; Pred. No. 2.4e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTGATTTCCCATTTAGCAGCTGCT 60
DB 18 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTGATTTCCCATTTAGCAGCTGCT 77
QY 61 TTTGGAATTTGACGTGATGAAAAATCCACATCAGATGACATGCTGCTGTTATTAT 120
DB 78 TTTGGAATTTGACGTGATGAAAAATCCACATCAGATGACATGCTGCTGTTATTAT 137
QY 121 GGCATTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 138 GGCATTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 197
QY 181 AAAATGAGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 198 AAAATGAGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 257
QY 241 CTGTATCTGACAGCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 300
DB 258 CTGTATCTGACAGCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 317
QY 301 TTTGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
DB 318 TTTGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 377
QY 361 ATCCCTTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 420
DB 378 ATCCCTTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 437
QY 421 TGCCTTTCCATTCACAAAATCGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 438 TGCCTTTCCATTCACAAAATCGATGATGATGATGATGATGATGATGATGATGATGAT 497
Y 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 498 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 557
QY 541 TCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 558 TCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 617
QY 601 ATTTGACTGACACTTCTTCTGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 660
DB 618 ATTTGACTGACACTTCTTCTGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 677
QY 661 ATTATTCACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
DB 678 ATTATTCACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 737
QY 721 AGGCTAACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
DB 738 AGGCTAACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 797
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DB 798 AGGCTAACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 857
QY 841 CATGAAGCTTACATGCTTTCTAGACCATTAAGTGTCTAACAACCTTTGTAACCTGTTA 900
DB 858 CATGAAGCTTACATGCTTTCTAGACCATTAAGTGTCTAACAACCTTTGTAACCTGTTA 917
QY 901 CATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 960

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DB 918 CATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT
QY 961 GTAGCGGAGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014
DB 978 GTAGCGGAGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1031

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RESULT 9
 ABL56198
 ID ABL56198 standard; DNA; 5435 BP.

AC ABL56198;
 DT 05-JUL-2002 (first entry)

DE Human P2Y1-11 encoding genomic sequence.

KW Human; P2Y1-11; chromosome 13; G protein-coupled; receptor;

KW gene therapy; thyroid; ds.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 318..4201

FT FT /tag- a /product- "P2Y1-like purine receptor"

PN DE10046970-A1.

PD 11-APR-2002.

PF 22-SEP-2000; 2000DE-1046970.

PR 22-SEP-2000; 2000DE-1046970.

PA (BRUE/) BRUESS M.

PA (BOEN/) BOENISCH H.

PI Bruess M, Boenisch H;

DR MPI; 2002-353329/39.

DR P-PSDB; ABB79438.

PT New human P2Y11 gene, useful for treatment and diagnosis of associated

PT diseases, and related proteins, antibodies and modulators, encodes G

PS protein-coupled receptor

PS Claim 1: Page 4-5; 5pp; German.

CC The invention relates to the human P2Y11 gene (I), including its 5' and

CC 3 untranslated regions, located on chromosome 13 and encoding a G

CC protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies

CC etc., are used for diagnosis and (gene) therapy of diseases that are

CC (indirectly associated with (I) or its expression products. No diseases

CC are specified but as (I) is expressed only in thyroid tissue, (I) is

CC presumed to be involved in regulation of thyroid function. The present

CC sequence is that of the P2Y11 encoding genomic sequence.

XX Sequence 5435 BP; 1509 A; 1168 C; 996 G; 1762 T; 0 other;

Query Match 99.8%; Score 1012.4; DB 24; Length 5435;
 Best Local Similarity 99.9%; Pred. No. 5e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTGATTTCCCATTTAGCAGCTGCT 60
DB 3188 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTGATTTCCCATTTAGCAGCTGCT 3247
QY 61 TTTGGAATTTGACGTGATGAAAAATCCACATCAGATGACATGCTGCTGTTATTAT 120
DB 3248 TTTGGAATTTGACGTGATGAAAAATCCACATCAGATGACATGCTGCTGTTATTAT 3307

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Db      8309 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTGTGATTTCCCGATTATGACAGCTGCT 8368
QY      61 TTTGGAAATTCACATGATGATAAAACATCCACTCAAGATGACTACTCTCCCTGTATTAT 120
Db      8369 TTTGGAAATTCACATGATGATAAAACATCCACTCAAGATGACTACTCTCCCTGTATTAT 8428
QY      121 GGCATTATCTCTGCTGGGATTTCCAGGCAATGAGATGATATCCACTTACATTTC 180
Db      8429 GGCATTATCTCTGCTGGGATTTCCAGGCAATGAGATGATATCCACTTACATTTC 8488
QY      181 AAAATGAGACCTTGAAGAGAGAGACACATCATTTATGCTGTAACCTGGCCCTGACAGATCTG 240
Db      8489 AAAATGAGACCTTGAAGAGAGAGACACATCATTTATGCTGTAACCTGGCCCTGACAGATCTG 8548
QY      241 CTGTATCTGACAGAGCTCCCTCTCTGATCTACTATGATGATGAGGCAAAACCTGGATC 300
Db      8549 CTGTATCTGACAGAGCTCCCTCTCTGATCTACTATGATGATGAGGCAAAACCTGGATC 8608
QY      301 TTTGGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Db      8609 TTTGGAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 8668
QY      361 ATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Db      8669 ATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8728
QY      421 TCTCTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db      8729 TCTCTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8788
QY      481 TCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db      8789 TCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 8848
QY      541 TCAGCTGTCTCTGACCTCAACAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db      8849 TCAGCTGTCTCTGACCTCAACAGTTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 8908
QY      601 ATTTGACTGCACTACTCTTCTGCTCCCTCTGATGATGATGATGATGATGATGATGATGATGATG 660
Db      8909 ATTTGACTGCACTACTCTTCTGCTCCCTCTGATGATGATGATGATGATGATGATGATGATGATG 8968
QY      661 ATTATCAACACTCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Db      8969 ATTATCAACACTCTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 9028
QY      721 AGGCTAACACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Db      9029 AGGCTAACACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 9088
QY      781 AGGCTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db      9089 AGGCTAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9148
QY      841 CATGAGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db      9149 CATGAGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9208
QY      901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db      9209 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9268
QY      961 GTAAAGCGGAACTTGAAGCAAGCAAAAGAAATTAAGTACTCAACACCTTTGA 1014
Db      9269 GTAAAGCGGAACTTGAAGCAAGCAAAAGAAATTAAGTACTCAACACCTTTGA 9322

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RESULT 11
 AAS08362
 ID AAS08362 standard; CDNA; 1729 BP.
 XX
 AC AAS08362;

```

XX      26-SEP-2001 (first entry)
XX      Human cDNA encoding G-protein coupled receptor, GPCR 39404.
DE      Human: G-protein coupled receptor; GPCR; 39404; Immunogen; antibody;
XX      Good pasture's syndrome; viral hepatitis; Alzheimer's disease; lymphoma;
KW      Heymann nephritis; Paget's disease; Crohn's disease; endometriosis;
KW      systemic lupus erythematosus; actinic keratosis; myocarditis;
KW      Kawasaki syndrome; DiGeorge syndrome; peripheral B-cell neoplasm;
KW      inflammations; teratoma; ss.
XX      Homo sapiens.
OS      Homo sapiens.
FH      Key
FT      Location/Qualifiers
FT      CDS
FT      294..1307
FT      /tag=a
FT      /product="Protein 39404"
XX      MO200149847-A2.
XX      12-JUL-2001.
XX      22-DEC-2000; 2000MO-US35309.
XX      30-DEC-1999; 99US-0475790.
XX      (MILL-) MILLENNIUM PHARM INC.
XX      Glucksmann MA, White D;
XX      MPI: 2001-432880/46.
XX      P-PSDB; AAU04584.
XX      Novel isolated 26904, 38911 and 39404 polypeptides which are seven
XX      transmembrane proteins belonging to superfamily of G-protein-coupled
XX      receptors, useful for treating disorders of spleen, lung, liver, brain
XX      and kidney -
XX      Claim 2; Fig 1; 164pp; English.
XX      The sequence encodes a novel human seven transmembrane domain
XX      protein belonging to the G-protein coupled receptor (GPCR) superfamily,
XX      protein 39404. The receptor is useful in drug screening assays, to
XX      identify compounds that modulate receptor activity and/or interact with
XX      the receptor, and for producing antibodies specific for the receptor, its
XX      regions or fragments. The receptor is useful for treating/diagnosing a
XX      aberrant expression or activity of the protein, for monitoring
XX      therapeutic effect during clinical trials and other treatment, as bait
XX      proteins in a two-hybrid or three-hybrid assay, and in pharmacogenomic
XX      analysis. The proteins and nucleic acids encoding them are useful for
XX      diagnosis and treatment of disorders selected from disorders of the
XX      spleen, lung such as Good pasture's syndrome, liver such as viral
XX      hepatitis, brain such as Alzheimer's disease, haematopoietic stem cells
XX      such as lymphoma, kidney such as Heymann nephritis, bone such as Paget's
XX      disease, colon such as Crohn's disease, uterus and endometrium such as
XX      endometriosis, T-cell disorders such as systemic lupus erythematosus,
XX      diseases of the skin such as actinic keratosis, disorders of the heart
XX      such as myocarditis, disorders involving blood vessels such as Kawasaki
XX      syndrome, disorders involving the thymus such as DiGeorge syndrome,
XX      disorders involving B-cells such as peripheral B-cell neoplasms,
XX      disorders of the breast such as inflammations, and disorders involving
XX      the testis and epididymis such as teratoma. Numerous examples of
XX      each type of disorder are given in the specification.
SO      Sequence 1729 BP; 461 A; 403 C; 302 G; 563 T; 0 other;

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Query Match 99.7%; Score 1010.8; DB 22; Length 1729;
 Best Local Similarity 99.8%; Pred. No. 8.2e-288;
 Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTGTGATTTCCCGATTATGACAGCTGCT 60


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Db      |||||||
294 ATGATAGGCGACAGACTATTTAGCAAAAGCTTCTATTTCCCGATTATGAGCGTCT 353
QY      |||||||
61 TTTGGAATTTGACTGATGAAACATCCCACTCAAGATGACCTACCCCGCTATTTAT 120
Db      |||||||
354 TTTGGAATTTGACTGATGAAACATCCCACTCAAGATGACCTACCCCGCTATTTAT 413
QY      |||||||
121 GGCATTATCTCTCTGCGGATTTCCAGGCAATGACAGTATGATATCCACTTATTTTC 180
Db      |||||||
414 GGCATTATCTCTCTGCGGATTTCCAGGCAATGACAGTATGATATCCACTTATTTTC 473
QY      |||||||
181 AAAATGAGACCTTGAGAGAGACACATATTTATGCTGAACCTGGCGCTGACAGATCTG 240
Db      |||||||
474 AAAATGAGACCTTGAGAGAGACACATATTTATGCTGAACCTGGCGCTGACAGATCTG 533
QY      |||||||
241 CTGTATCTGACAGACCTCTCCCTTCTATTTCACTACTATGCGATGCGAGAAATCTGATC 300
Db      |||||||
534 CTGTATCTGACAGACCTCTCCCTTCTATTTCACTACTATGCGATGCGAGAAATCTGATC 593
QY      |||||||
301 TTTGAGATTTTCACTGTTAAGTTTATCCGCTTACGCTTCAATTTCAACCTGTATAGAGC 360
Db      |||||||
594 TTTGAGATTTTCACTGTTAAGTTTATCCGCTTACGCTTCAATTTCAACCTGTATAGAGC 653
QY      |||||||
361 ATCCCTTCTCCACCTGTTTACAGATCTCCGCTACTGCTGATGATTCACCCATGAGC 420
Db      |||||||
654 ATCCCTTCTCCACCTGTTTACAGATCTCCGCTACTGCTGATGATTCACCCATGAGC 713
QY      |||||||
421 TGCCTTTCATTCACAAACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 480
Db      |||||||
714 TGCCTTTCATTCACAAACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 773
QY      |||||||
481 TCACGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 540
Db      |||||||
774 TCACGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 833
QY      |||||||
541 TCAGCCGTGCTGACCTGACAGTGGATGGAATCACTAATTAAGTGTATTAACCTA 600
Db      |||||||
834 TCAGCCGTGCTGACCTGACAGTGGATGGAATCACTAATTAAGTGTATTAACCTA 893
QY      |||||||
601 ATTTGACTGCACTACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db      |||||||
894 ATTTGACTGCACTACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 953
QY      |||||||
661 ATTATTCACACTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db      |||||||
954 ATTATTCACACTGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1013
QY      |||||||
721 AGGCTAACCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db      |||||||
1014 AGGCTAACCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073
QY      |||||||
781 AGGCTAACCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db      |||||||
1074 AGGCTAACCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1133
QY      |||||||
841 CATTGAGCTTACATGCTTTCTAGACATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db      |||||||
1134 CATTGAGCTTACATGCTTTCTGACATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1193
QY      |||||||
901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db      |||||||
1194 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253
QY      |||||||
961 GTAAGGGGGAACCTTGAGCAAGCAAAAGAAATTAAGTACTCAAAACACCTTGA 1014
Db      |||||||
1254 GTAAGGGGGAACCTTGAGCAAGCAAAAGAAATTAAGTACTCAAAACACCTTGA 1307

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RESULT 12
 ABV24026
 ID ABV24026 standard; cdna; 1729 BP.
 XX
 AC ABV24026;

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XX      16-SEP-2002 (first entry)
DT
XX      Human prostate expression marker cDNA 24017.
DE
XX      Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW      pharmacogenomic marker; gene; ss.
OS      Homo sapiens.
XX      WO200160860-A2.
XX      23-AUG-2001.
XX      20-FEB-2001; 2001WO-US05171.
XX      17-FEB-2000; 2000US-183319P.
XX      16-MAR-2000; 2000US-189862P.
XX      25-MAY-2000; 2000US-207454P.
XX      09-JUN-2000; 2000US-211314P.
XX      18-JUL-2000; 2000US-219007P.
XX      13-DEC-2000; 2000US-255281P.
XX
XX      (MILL-) MILENNIUM PREDICTIVE MEDICINE INC.
XX      Schlegel R, Endege WO, Monahan JE;
XX      WPI; 2001-662795/76.
XX
XX      Novel isolated nucleic acid molecule associated with cancerous state of
XX      prostate cells and correlating with presence of prostate cancer, useful
XX      for detecting presence of prostate cancer, stage of prostate cancer
XX      Claim 1; Page 4453-4454; 11750pp; English.
XX
XX      The invention relates to an isolated nucleic acid molecule (I) comprising
XX      a nucleotide sequence given in Tables 1-9 (ABV00010-ABV22213) of the
XX      specification or its complement. (I) is useful for:
XX      (a) assessing whether a patient is afflicted with prostate cancer;
XX      (b) monitoring the progression of prostate cancer in a patient;
XX      (c) assessing the efficacy of a test compound to inhibit prostate
XX      cancer in a patient;
XX      (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX      in a patient;
XX      (e) selecting a composition for inhibiting prostate cancer in a patient;
XX      (f) assessing the prostate cell carcinogenic potential of a compound;
XX      (g) determining whether prostate cancer has metastasized in a patient;
XX      (h) assessing the aggressiveness or indolence of prostate cancer in a
XX      patient;
XX      (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX      Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;
SQ

```

Query Match 99.7%; Score 1010.8; DB 23; Length 1729;
 Best Local Similarity 99.8%; Pred. No. 8.2e-288;
 Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY      1 ATGATAGGCGACAGACTATTTAGCAAAAGCTTCTATTTCCCGATTATGAGCGTCT 60
Db      |||||||
294 ATGATAGGCGACAGACTATTTAGCAAAAGCTTCTATTTCCCGATTATGAGCGTCT 353
QY      |||||||
61 TTTGGAATTTGACTGATGAAACATCCCACTCAAGATGACCTACCCCGCTATTTAT 120
Db      |||||||
354 TTTGGAATTTGACTGATGAAACATCCCACTCAAGATGACCTACCCCGCTATTTAT 413
QY      |||||||
121 GGCATTATCTCTCTGCGGATTTCCAGGCAATGACAGTATGATATCCACTTATTTTC 180
Db      |||||||
414 GGCATTATCTCTCTGCGGATTTCCAGGCAATGACAGTATGATATCCACTTATTTTC 473
QY      |||||||
181 AAAATGAGACCTTGAGAGAGACACATATTTATGCTGAACCTGGCGCTGACAGATCTG 240
Db      |||||||
474 AAAATGAGACCTTGAGAGAGACACATATTTATGCTGAACCTGGCGCTGACAGATCTG 533

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QY 481 TCACGTGAGCTGTCATTCGATGACCTTCTGTATCATCAACCAAGAGACCAAGAGA 540
 DB 774 TCACGTGAGCTGTCATTCGATGACCTTCTGTATCATCAACCAAGAGACCAAGAGA 833
 QY 541 TCAGCCGTGTCGACCTCACCAGTTCGGATGAACTCAATATTAAGTGTACACCTA 600
 DB 834 TCAGCCGTGTCGACCTCACCAGTTCGGATGAACTCAATATTAAGTGTACACCTG 893
 QY 601 ATTTGACTGCACTACTTCTGCTCCCTGCTGGTATGATGACACTTTGTATACACG 660
 DB 894 ATTTGACTGCACTACTTCTGCTCCCTGCTGGTATGATGACACTTTGTATACACG 953
 QY 661 ATTATCCACACTGTGACCCATGAGACTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGA 720
 DB 954 ATTATCCACACTGTGACCCATGAGACTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGA 1013
 QY 721 AGGCTAACCATTTCTGCTACTCTTGTGCAATTTAGTATGTTTATACCTTCCATATCTTG 780
 DB 1014 AGGCTAACCATTTCTGCTACTCTTGTGCAATTTAGTATGTTTATACCTTCCATATCTTG 1073
 QY 781 AGGCTAACCATTTCTGCTACTCTTGTGCAATTTAGTATGTTTATACCTTCCATATCTTG 840
 DB 1074 AGGCTAACCATTTCTGCTACTCTTGTGCAATTTAGTATGTTTATACCTTCCATATCTTG 1133
 Y 841 CATGACCTTACATCTGTTTCTAGACATTAAGCTGCTGTGAACACCTTTGGTAACTCTGTA 900
 DB 1134 CATGACCTTACATCTGTTTCTAGACATTAAGCTGCTGTGAACACCTTTGGTAACTCTGTA 1193
 QY 901 CTATATGCTGTGTCGACGCAACCTTTCACAGGCTGTCGCTCAACAGTGAATGCAAA 960
 DB 1194 CTATATGCTGTGTCGACGCAACCTTTCACAGGCTGTCGCTCAACAGTGAATGCAAA 1253
 QY 961 GTAAGCGGAACCTTGAGCAAGCAAGAAATTAAGTACTCAAAACACCTTGA 1014
 DB 1254 GTAAGCGGAACCTTGAGCAAGCAAGAAATTAAGTACTCAAAACACCTTGA 1307

RESULT 14
 ABV29909
 ID ABV29909 standard; cDNA; 1729 BP.
 XX
 AC ABV29909;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 29900.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001MO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 23-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 PS Claim 1; Page 6451; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SO Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;
 Query Match 99.7%; Score 1010.8; DB 23; Length 1729;
 Best Local Similarity 99.8%; Pred. No. 8.2e-288;
 Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAATGAGCAGCAGTATATTTAGCAAACTCTGATTTCCCGATTAAGCAGCTGCT 60
 DB 294 ATGAATGAGCAGCAGTATATTTAGCAAACTCTGATTTCCCGATTAAGCAGCTGCT 353
 QY 61 TTGGAAATTTGCACTGATGAAGAAATCCACTCAAGATGACACTGCTCCGTATTTAT 120
 DB 354 TTGGAAATTTGCACTGATGAAGAAATCCACTCAAGATGACACTGCTCCGTATTTAT 413
 QY 121 GGCAATTTCTTCCCTCGGGGATTTCCAGGCAATGCAATGATGATATCCACTTATTTTC 180
 DB 414 GGCAATTTCTTCCCTCGGGGATTTCCAGGCAATGCAATGATGATATCCACTTATTTTC 473
 QY 181 AAATGAGACCTTGGAGAGAGCAGCAGCATCTATATGCTGAACCTGGCGTGCAGATCTG 240
 DB 474 AAATGAGACCTTGGAGAGAGCAGCAGCATCTATATGCTGAACCTGGCGTGCAGATCTG 533
 QY 241 CTGATCTGACACAGCTCCCTTCGATTCATCTACTATGACAGTGGCAAACTGATC 300
 DB 534 CTGATCTGACACAGCTCCCTTCGATTCATCTACTATGACAGTGGCAAACTGATC 593
 QY 301 TTGGGAATTTCAATGATTAAGTTATCCGCTTCAGCTTCCATTTCAACCTGATAGCAGC 360
 DB 594 TTGGGAATTTCAATGATTAAGTTATCCGCTTCAGCTTCCATTTCAACCTGATAGCAGC 653
 QY 361 ATTCCTTCCGACCTGTTTCAGACATCTCCGCTGACTGTGATGATTCACCCCAATAGC 420
 DB 654 ATTCCTTCCGACCTGTTTCAGACATCTCCGCTGACTGTGATGATTCACCCCAATAGC 713
 QY 421 TGCCTTTTCATTCACAAACTCGATGTGACAGTTGTACCTGCTGTGTGTGATCAT 480
 DB 714 TGCCTTTTCATTCACAAACTCGATGTGACAGTTGTACCTGCTGTGTGTGATCAT 773
 QY 481 TCACGTGAGCTGTCATTCGATGACCTTCTGTATCATCAACCAAGAGACCAAGAGA 540
 DB 774 TCACGTGAGCTGTCATTCGATGACCTTCTGTATCATCAACCAAGAGACCAAGAGA 833
 QY 541 TCAGCCGTGTCGACCTCACCAGTTCGGATGAACTCAATATTAAGTGTACACCTA 600
 DB 834 TCAGCCGTGTCGACCTCACCAGTTCGGATGAACTCAATATTAAGTGTACACCTG 893
 QY 601 ATTTGACTGCACTACTTCTGCTCCCTGCTGGTATGATGACACTTTGTATACACG 660
 DB 894 ATTTGACTGCACTACTTCTGCTCCCTGCTGGTATGATGACACTTTGTATACACG 953
 QY 661 ATTATCCACACTGTGACCCATGAGACTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGA 720

Db 954 ATTATCCACACTCTGACCATGAGCTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGA 1013
 Qy 721 AGGCTAACATCTCTGCTACTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 780
 Db 1014 AGGCTAACATCTCTGCTACTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 1073
 Qy 781 AGGCTAACATCTCTGCTACTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 840
 Db 1074 AGGCTAACATCTCTGCTACTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 1133
 Qy 841 CATGAAGCTTACATCTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 900
 Db 1134 CATGAAGCTTACATCTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 1193
 Qy 901 CTATATGTGTGTGTGTCAGCAGCACTTTTACAGAGGCTGTCTGCAACAGTGAATGCAAA 960
 Db 1194 CTATATGTGTGTGTGTCAGCAGCACTTTTACAGAGGCTGTCTGCAACAGTGAATGCAAA 1253
 Qy 961 GTAAAGCGGACCTTGAAGCAGCAAAATAATTAGTTACTCAAAACCTTGA 1014
 Db 1254 GTAAAGCGGACCTTGAAGCAGCAAAATAATTAGTTACTCAAAACCTTGA 1307

 RESULT 15
 ABV30024
 ID ABV30024 standard; cDNA; 1729 BP.
 XX
 AC ABV30024;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 30015.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 XX
 PN MO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001MO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 DR MPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 PS Claim 1; Page 6487-6488; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other:

 Query Match 99.7%; Score 1010.8; DB 23; Length 1729;
 Best Local Similarity 99.8%; Pred. No. 8.2e-288;
 Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 1 ATGAATGAGCCTTACATCTTATGCAAAATCTTGTATTTCCCGATTTAGAGCTGT 60
 Db 294 ATGAATGAGCCTTACATCTTATGCAAAATCTTGTATTTCCCGATTTAGAGCTGT 353
 Qy 61 TTGGAATTTGCACTGATGAAACATCCCATCAAGATGACATCTCCCTGTTATTTAT 120
 Db 354 TTGGAATTTGCACTGATGAAACATCCCATCAAGATGACATCTCCCTGTTATTTAT 413
 Qy 121 GGCATTATCTCTCTGATTTCCAGCAATGACATGATGATATTCATTTTC 180
 Db 414 GGCATTATCTCTCTGATTTCCAGCAATGACATGATGATATTCATTTTC 473
 Qy 181 AAATGAGACCTTGAAGAGCAGCACCACATCATATCTGAACTGGCTGACAGATCTG 240
 Db 474 AAATGAGACCTTGAAGAGCAGCACCACATCATATCTGAACTGGCTGACAGATCTG 533
 Qy 241 CTGTATCTGACAGCCTCCCTCTCTGATTTCACTACTATGACAGTGGCGAAATCTGAT 300
 Db 534 CTGTATCTGACAGCCTCCCTCTCTGATTTCACTACTATGACAGTGGCGAAATCTGAT 593
 Qy 301 TTGGAATTTGCACTGATGAAACATCCCATCAAGATGACATCTCCCTGTTATTTAT 360
 Db 594 TTGGAATTTGCACTGATGAAACATCCCATCAAGATGACATCTCCCTGTTATTTAT 653
 Qy 361 ATCCCTCTCTGACATCTTCCAGATCTTCCAGATCTTCCAGATCTTCCAGATCTTCCAG 420
 Db 654 ATCCCTCTCTGACATCTTCCAGATCTTCCAGATCTTCCAGATCTTCCAGATCTTCCAG 713
 Qy 421 TGCTTTTCATTCACAAACCTGATGAGTGTGAGCTGTGCTGTGATTCAT 480
 Db 714 TGCTTTTCATTCACAAACCTGATGAGTGTGAGCTGTGCTGTGATTCAT 773
 Qy 481 TCACCTGTGATCTATTCGATGAGTGTGATGATGATGATGATGATGATGATGATGATG 540
 Db 774 TCACCTGTGATCTATTCGATGAGTGTGATGATGATGATGATGATGATGATGATGATG 833
 Qy 541 TCACCTGTGATCTATTCGATGAGTGTGATGATGATGATGATGATGATGATGATGATG 600
 Db 834 TCACCTGTGATCTATTCGATGAGTGTGATGATGATGATGATGATGATGATGATGATG 893
 Qy 601 ATTTGACTGCAACTCTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 Db 894 ATTTGACTGCAACTCTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 953
 Qy 661 ATTTGACTGCAACTCTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 Db 954 ATTTGACTGCAACTCTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1013
 Qy 721 AGGCTAACATCTCTGCTACTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 780
 Db 1014 AGGCTAACATCTCTGCTACTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 1073
 Qy 781 AGGCTAACATCTCTGCTACTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 840
 Db 1074 AGGCTAACATCTCTGCTACTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 1133
 Qy 841 CATGAAGCTTACATCTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 900
 Db 1134 CATGAAGCTTACATCTCTCTGATTTTATGTTTATTTTACCCTCCATTCCTG 1193
 Qy 901 CTATATGTGTGTGTGTCAGCAGCACTTTTACAGAGGCTGTCTGCAACAGTGAATGCAAA 960

Db 1194 CTATATGTGTGTGCAGGCACTTCAGCAGGCTGTCTCTCAGAGTGAGATGCAAA 1253
OY 961 GTAAGCGGGAACCTTTGAGCAAGCAAAATTTAGTTACTCAACCAACCCCTTGA 1014
Db 1254 GTAAGCGGGAACCTTTGAGCAAGCAAAATTTAGTTACTCAACCAACCCCTTGA 1307

Search completed: May 29, 2003, 22:24:06
Job time : 306 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 29, 2003, 23:45:11 ; Search time 199 Seconds

(without alignments)
2283.412 Million cell updates/sec

Title: US-10-023-775B-2

Perfect score: 1771

Sequence: 1 MNEPLDYIANNADPEPDYAAA.....RCKVSGNLEQAKISYSNNP 337

Scoring table:

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Xgapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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Database : Published Applications_NA:*

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than, or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1771	100.0	1014 9	US-10-023-775B-1
2	1771	100.0	1014 9	US-10-270-144-1
3	1771	100.0	1014 9	US-10-188-405-7
4	1771	100.0	1014 9	US-09-885-453-2

5	1771	100.0	1014 10	US-09-943-798-3	Sequence 3, Appli
6	1771	100.0	9020 9	US-10-270-144-3	Sequence 3, Appli
7	1724	97.3	1020 9	US-09-782-974C-85	Sequence 85, Appli
8	1444	81.5	831 10	US-09-943-798-1	Sequence 1, Appli
9	1279.5	72.2	1313 10	US-09-728-422-1	Sequence 1, Appli
10	940	53.1	578 9	US-09-782-974C-59	Sequence 59, Appli
11	915	51.7	526 10	US-09-812-102-40	Sequence 40, Appli
12	514	29.0	1429 9	US-09-071-173A-1	Sequence 1, Appli
13	488	27.6	1428 9	US-10-270-587-1	Sequence 1, Appli
14	487.5	27.5	993 10	US-09-826-791-1	Sequence 1, Appli
15	487.5	27.5	1041 9	US-09-828-478-1	Sequence 1, Appli
16	487.5	27.5	1041 10	US-09-826-791-5	Sequence 5, Appli
17	487.5	27.5	1041 10	US-09-866-230-6	Sequence 6, Appli
18	487.5	27.5	1260 9	US-09-779-679-1	Sequence 1, Appli
19	487.5	27.5	1260 9	US-09-779-679-24	Sequence 24, Appli
20	487.5	27.5	1430 9	US-09-828-478-3	Sequence 3, Appli
21	487.5	27.5	1700 10	US-09-728-952-26	Sequence 26, Appli
22	426	24.1	1543 9	US-09-891-138A-1	Sequence 1, Appli
23	397	22.4	2577 9	US-09-966-755-1	Sequence 1, Appli
24	397	22.4	2577 10	US-09-903-377-1	Sequence 1, Appli
25	397	22.4	2577 10	US-09-952-385-1	Sequence 1, Appli
26	397	22.4	2577 12	US-10-000-759A-1	Sequence 1, Appli
27	394.5	22.3	1020 10	US-09-788-133-1	Sequence 1, Appli
28	388.5	21.9	3299 9	US-10-208-408-24	Sequence 24, Appli
29	379.5	21.4	1017 9	US-09-885-453-3	Sequence 3, Appli
30	375.5	21.2	1080 10	US-09-739-151-1	Sequence 1, Appli
31	375.5	21.2	1425 9	US-10-094-417-9	Sequence 9, Appli
32	375.5	21.2	2137 9	US-09-782-974C-75	Sequence 75, Appli
33	371	20.9	1065 9	US-09-922-895-2	Sequence 2, Appli
34	371	20.9	1717 10	US-09-964-824A-100	Sequence 100, App
35	371	20.9	1915 12	US-10-106-623-3	Sequence 3, Appli
36	371	20.9	3426 9	US-10-001-835-29	Sequence 29, Appli
37	370.5	20.9	1955 9	US-10-190-489-2	Sequence 2, Appli
38	370	20.9	1689 10	US-09-931-381A-15	Sequence 15, Appli
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40	354	20.0	1737 9	US-09-104-063-3	Sequence 3, Appli
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42	351	19.8	1358 9	US-10-167-192-4	Sequence 4, Appli
43	348	19.6	1102 9	US-09-870-759-143	Sequence 143, App
44	348	19.6	2693 9	US-09-850-948-1	Sequence 1, Appli
45	347	19.6	1014 9	US-09-850-948-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-023-775B-1
; Sequence 1, Application US/10023775B
; Publication No. US20030022282A1
GENERAL INFORMATION:
APPLICANT: Pfizer Ltd. (EP/GB only)
APPLICANT: Pfizer Inc. (US, JP, EB except GB)
APPLICANT: Fidock, Mark David
TITLE OF INVENTION: No. US20030022282A1 Polypeptide
FILE REFERENCE: PC10959ACPR
CURRENT APPLICATION NUMBER: US/10/023,775B
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: GB 0030854.4
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/260,590
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: US 60/296,660
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: GB 0111031.1
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1014
TYPE: DNA
ORGANISM: Homo sapiens
US-10-023-775B-1

Alignment Scores:

Pred. No.:	1,5e-158	Length:	1014
Score:	1771.00	Matches:	337
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-023-775B-2 (1-337) x US-10-023-775B-1 (1-1014)

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QY 1 MetAsnGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAlaAla 20
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Db 1 ATGAATGAGACCTTGAAGAGACACCATATTATGCTGAACCTGGCTGACAGATCTG 60
QY PheGlyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
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QY 41 GlyTleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
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Db 181 AAATATGAGACCTTGAAGAGACACCATATTATGCTGAACCTGGCTGACAGATCTG 240
QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrAlaSerGlyIleAsnTyrPile 100
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Db 241 CTGTATCTGACGACCTCCCTCCCTGATTCACATGATTCAGTGGCAAACTGGATC 300
QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
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QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSer 140
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QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTyrPileIle 160
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Db 421 TGCTTTCCATTCACAAACTCGATGCGATGCGATGCGATGCGATGCGATGCGAT 480
QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
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Db 481 TCACGTGACCTGCTGATTCGATGACCTGCTGATGACCTGCTGATGACCTGCT 540
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Db 541 TCAGCTGCTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 600
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QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
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QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
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Db 721 AGGCTATACCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
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RESULT 2

US-10-270-144-1

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; Sequence 1, Application US/10270144
; Publication No. US20030049790A1
; GENERAL INFORMATION:
; APPLICANT: MET, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000750CON
; CURRENT APPLICATION NUMBER: US/10/270,144
; PRIOR APPLICATION NUMBER: 2002-10-15
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Human
; US-10-270-144-1

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Alignment Scores:

Pred. No.:	1,5e-158	Length:	1014
Score:	1771.00	Matches:	337
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-023-775B-2 (1-337) x US-10-270-144-1 (1-1014)

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QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyIleAsnTyrPile 100
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Db 241 CTGTATCTGACGACCTCCCTCCCTGATTCACATGATTCAGTGGCAAACTGGATC 300
QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
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Db 301 TTGGAAATTTGACCTATGATAAATCCACATGACATGACATGATTTAT 360
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   |||
Db 361 ATCCCTCTCTCCACCTGTTTCACACATCTCCGCTGATGCTGATTCATCCCAAGAGC 420
QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTyrPileIle 160
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Db 421 TGCTTTCCATTCACAAACTCGATGCGATGCGATGCGATGCGATGCGATGCGAT 480
QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
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 QY 201 IleLeuThrAlaThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
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 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
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 DB 901 CTATATGT 960
 QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
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RESULT 3

US-10-188-405-7
 ; Sequence 7, Application US/10188405
 ; Publication No. US20030082585A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tian, Hui
 ; APPLICANT: Dai, Kang
 ; APPLICANT: Chen, Jin-Long
 ; APPLICANT: Zhao, Jiagang
 ; APPLICANT: Cutler, Gene
 ; APPLICANT: Tularik Inc.
 ; TITLE OF INVENTION: No. US20030082585A1el Receptors
 ; FILE REFERENCE: 018781-008410US
 ; CURRENT APPLICATION NUMBER: US/10/188,405
 ; CURRENT FILING DATE: 2002-07-01
 ; PRIOR APPLICATION NUMBER: US 60/302,800
 ; FILING DATE: 2001-07-03
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 1014
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human TGR164
 US-10-188-405-7

Alignment Scores:

Pred. No.: 1.5e-158 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservatve: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-023-775B-2 (1-337) x US-10-188-405-7 (1-1014)

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QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
 DB 61 TTGGAAATTCGACCTGATGAAAACATCCACATCAAGATGACACTACTCTCTTATTAT 120
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 121 GGCATTATCTCTCTGTTGGGATTCAGGCAATGCAAGATGATATTCACACTTACATTTTC 180
 QY 61 LysMetArgProTrpLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 181 AAAATGAGACCTTGAGAGAGAGACACATCATATATGCAAGCTGCTGCAAGATCTG 240
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyLysAsnTrpIle 100
 DB 241 CTGTATCTGACCAAGCTCCCTCTCTGATTCCTACTATGCAAGGCGGAAAAACGATC 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisAspAsnLeuTyrSerSer 120
 DB 301 TTGGAGATTTTCATGTGTAAGTTATCCGCTTCACCTTCATTCACCTGATATGACAGC 360
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 DB 361 ATCCCTCTCTCACCCTGTTTACGATCTCCCTCTCTGATCATTCACCAATGAGC 420
 QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValIleTrpIleIle 160
 DB 421 TGCCTTTTCATTCACAAAACCTGATGTGACGTGATGCTGTGCTGTGCTGTGATCATT 480
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCAGTGTAGCTGATTCATTCGATGACCTCTTCATGATCATCATCAACCAAGAGCAAGCA 540
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTyrAsnLeu 200
 DB 541 TCAGGCTGCTGCGACCTCAGGATTCGAGTGAACCACTATTATTAAGGGTACCACTG 600
 QY 201 IleLeuThrAlaThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 601 ATTTGACTGCAACTACTTTCTGCTCCCTGGGATGATGACACTTTGCTATACCAAG 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 661 ATTATCCACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 720
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 721 AGGCTAACCATCTCTCTACTCTTGCATTTTACGATGTGTTTTCCTTCATATCTTG 780
 QY 261 ArgValIleArgIleGluSerArgLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 781 AGGCTCATTCGATCGAATCTGCTGCTTCATCAATGATGTTTCCATGAGATCAGATC 840
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 841 CATGAGCTTACATGCTTCTAGACCATTAAGCTGCTGACACACCTTGGTAACTGTTA 900
 QY 301 LeuTyrValIleValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGT 960
 QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 961 GTAAGCGGGAACCTTGAGCAAGCAAGAAATAATTAGTACTCAACACACCT 1011

RESULT 4

US-09-885-453-2
 ; Sequence 2, Application US/09885453
 ; Publication No. US20030088080A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Communt, Didier
 ; TITLE OF INVENTION: RECEPTOR GPCRxi10
 ; FILE REFERENCE: 9409/2082
 ; CURRENT APPLICATION NUMBER: US/09/885,453

; CURRENT FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: US 09/885,453
 ; PRIOR FILING DATE: 2001-06-21
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 1014
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DNA nucleotide sequence
 ; LOCATION: (1)..(1014)
 ; OTHER INFORMATION: GPCR10 DNA sequence
 ; US-09-885-453-2

Alignment Scores:
 Pred. No.: 1,5e-158 length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-023-775b-2 (1-337) x US-09-885-453-2 (1-1014)

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 QY 21 Pheglvasncysrhspgluasnlleproleuylsmethistyrleuprovallietyr 40
 61 TTTGGAATTCGACTGATGAAAACATCCACTCAAGATGCACTCCCTGTTATTAT 120
 QY 41 Glyllelepheleuvalglypheproglyasnalavalalleserthryrilephe 60
 121 GGCATTATCTTCTCCTCGGGATTTCCAGCAATGCACTAGTATCCACTTTCATTTTC 180
 QY 61 LysmetargprotrpilyserSerthrllellemetleuansleualacysrhspheu 80
 181 AAATGAGACCTTGGAGAGACAGACCATCATTTATGCTGAACCTGGCTGCAGACATCTG 240
 QY 81 Leutyrlleuhrsleuupropheullehstyrtyrralaserglyluasntprile 100
 241 CTGATCTGACACCTCCCTCCCTGATTCACATCATCCAGTCCGAAACTGATC 300
 QY 101 PheglvaspphemecylsypheilleargpheSerphesleuansleuTyrsSer 120
 301 TTGGAGATTTCATGTTATGATTCAGCTTCAGCTTCATTTCAACCTGTATAGCAGC 360
 QY 121 IleleuhsleuhrsCyspheSerllepheargtyrcysvalillelehisPrometSer 140
 361 ATCCCTTCTCCTCAGCTTTCAGCATCTCCGCTAGCTGATCATTCACCCCAATGAGC 420
 QY 141 CyspheSerllehissthrargcysalavalalacysalavalatprille 160
 421 TGGCTTTCCTACAACTCGATGAGTGTGTACCTGCTGGTGGTGTGATATT 480
 QY 161 Serleuvalalavalileprometthrpheleullehserthrasnargthrasnarg 180
 481 TCACGTGATCTGCTCATTCGATGACCTTCTGATCATCATCAACCAAGACCAACAGA 540
 QY 181 Serleuvalalavalileprometthrpheleullehserthrasnargthrasnarg 200
 541 TCAGCCGTCTGACACCTGACAGTGTGATGAGTGTGATGATGATGATGATGATGATG 600
 QY 201 Ileleuhsleuhrsleuupropheullehstyrtyrralaserglyluasntprile 220
 601 ATTTGAGTCACTGATCTTCTGCTCCCTGCTGATGATGATGATGATGATGATGATGATG 660
 QY 221 Ilelehissthrleuhrsleuupropheullehstyrtyrralaserglyluasntprile 240
 661 ATTTGAGTCACTGATCTTCTGCTCCCTGCTGATGATGATGATGATGATGATGATGATG 720

QY 241 Argleuhsrthlleleuhsleuupropheullehstyrtyrralaserglyluasntprile 260
 721 AGGCTAACCATTCTGCTACCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 780
 QY 261 Argvalillearglleuhsleuupropheullehstyrtyrralaserglyluasntprile 280
 781 AGGCTAACCATTCTGCTACCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 840
 QY 281 HisglualatryllevalSerargproleualaalaaleuansleuhsleuupropheulleh 300
 841 CATGAGCTTACATCTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 900
 QY 301 LeutyrrvalavalSerasphepneinglnalavalCysSerthryrvalargcyls 320
 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 321 ValSerglynsleuuglnalalylsleSerthryrvalargcyls 337
 961 GTAAGCGGGAACCTTGGAGAGCAAGCAAAATTAATGATCAAAACACCT 1011

RESULT 5

US-09-943-798-3

; Sequence 3, Application US/09943798
 ; Patent No. US20020065215A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glaxo Group Limited
 ; TITLE OF INVENTION: Polypeptide
 ; FILE REFERENCE: 061021
 ; CURRENT APPLICATION NUMBER: US/09/943,798
 ; CURRENT FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 1014
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-943-798-3

Alignment Scores:
 Pred. No.: 1,5e-158 length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-023-775b-2 (1-337) x US-09-943-798-3 (1-1014)

QY 1 Metasngluproleuasptrylleualaasnlaseraspheproasptryllaalaala 20
 1 ATGATGAGCCACTAGACTATTGAGCAATGCTTCGATTTCCCGCATTTATGACGCTGCT 60
 QY 21 Pheglvasncysrhspgluasnlleproleuylsmethistyrleuprovallietyr 40
 61 TTTGGAATTCGACTGATGAAAACATCCACTCAAGATGCACTCCCTGTTATTAT 120
 QY 41 Glyllelepheleuvalglypheproglyasnalavalalleserthryrilephe 60
 121 GGCATTATCTTCTCCTCGGGATTTCCAGCAATGCACTAGTATCCACTTTCATTTTC 180
 QY 61 LysmetargprotrpilyserSerthrllellemetleuansleualacysrhspheu 80
 181 AAATGAGACCTTGGAGAGACAGACCATCATTTATGCTGAACCTGGCTGCAGACATCTG 240
 QY 81 Leutyrlleuhrsleuupropheullehstyrtyrralaserglyluasntprile 100
 241 CTGATCTGACACCTCCCTCCCTGATTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 QY 101 PheglvaspphemecylsypheilleargpheSerphesleuansleuTyrsSer 120
 301 TTGGAGATTTCATGTTATGATTCAGCTTCAGCTTCATTTCAACCTGTATAGCAGC 360
 QY 121 IleleuhsleuhrsCyspheSerllepheargtyrcysvalillelehisPrometSer 140


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|||||
Db 361 ATCCCTTCCTCACCCTGTTGACGACTTCCGCTACTGCTGATCATTCACCAATGAGC 420
QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaAlaCysAlaValAlaIle 160
Db 421 TCCCTTTCATTCACAAAACCTGATGCTGAGTGTGAGCTGCTGCTGCTGCTGCTGCT 480
QY 161 SerLeuValAlaValAlaIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
Db 481 TCACGTGAGCTGTATTCCTGATCCGATCTTCTTGATCATCATCAACCAAGGACCAACAGA 540
QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTyrAsnLeu 200
Db 541 TCAGCTGCTGCTGACCTGACAGCTTCGATGATCAATCAATATTAAGTGAACAACCTG 600
QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
Db 601 ATTTTGACGTGACAACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
Db 661 ATTATCCACACTCTACCCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAAGACAGA 720
QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheThrValCysPheLeuProPheHisIleLeu 260
Db 721 AGGCTAACCATCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 261 ArgValIleArgIleGluSerArgLeuSerIleSerCysSerIleGluAsnGlnIle 280
Db 781 AGGGTCATTCGGATGGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 281 HisGluAlaThrIleValSerArgProLeuAlaIleAlaLeuAsnThrPheGlyAsnLeu 300
Db 841 CATGAAGCTTACATGCTTCTAGACCATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 301 LeuThrValAlaValSerAspAsnPheGlnAlaValCysSerThrValArgCysLys 320
Db 901 CTATATGTGTGTGTGCTGAGCAGCAAACTTTCAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 321 ValSerGlyAsnLeuGlnAlaValLysLysIleSerTyrSerAsnAsnPro 337
Db 961 GTAAAGGGGAACTTGGAGCAAGCAAAATAATTAAGTCAAAACCAACCT 1011

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RESULT 6

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US-10-270-144-3
; Sequence 3, Application US/10270144
; Publication No. US20030049790A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00750CON
; CURRENT APPLICATION NUMBER: US/10/270,144
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9905
; TYPE: DNA
; ORGANISM: Human
US-10-270-144-3

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Alignment Scores:

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Pred. No.: 4,07e-157 Length: 9905
Score: 1771.00 Matches: 337
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

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US-10-023-775b-2 (1-337) x US-10-270-144-3 (1-9905)

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QY 1 MetAsnGluProLeuAspTyrIleuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
Db 8309 ATGAATGAGCCACTACACTATTTAGCAAAATGCTTGTGATTTCCCGCATTAATACAGCTGCT 8368
QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisTyrIleuProValIleTyr 40
Db 8369 TTGGGAATATGCACATGATAAAAACATCCCACTCAAGATCATCTACTCCCTGTATTATT 8428
QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValAlaIleSerThrTyrIlePhe 60
Db 8429 GGCATTATCTCTCGTGGGATTTCCAGCAATGAGTAGATATATCCACTATACATTTC 8488
QY 61 LysMetArgProTrpLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
Db 8489 AAAATGAGACCTTGGAAAGAGCAGCAACATATTAAGCTGAACCTGGCCGCGACAAATCTG 8548
QY 81 LeuThrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyLysAsnTrpIle 100
Db 8549 CTGTATCTGACAGCCCTCCCTCTGATTCCTACTATGCAATGCGCAAAACCTGATC 8608
QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
Db 8609 TTGGAGATTTTCATGTGTAAGTTATCCGCTTACAGCTTCATTCACCTGTAATGAGCAGC 8668
QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
Db 8669 ATCCCTTCCTCACCCTGTTTCAGCAATCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8728
QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaAlaCysAlaValAlaIleIle 160
Db 8729 TCCCTTTCATTCACAAAACCTGATGCTGAGTGTGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 8788
QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
Db 8789 TCACGTGAGCTGTATTCCTGATCCGATGACCTTGTGATCATCATCAACCAAGCAGCAACAGA 8848
QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTyrAsnLeu 200
Db 8849 TCAGCTGCTGCTGACCTCACCAGTTCGATGAGCAATCAATATTAAGGAGTCAACCTG 8908
QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
Db 8909 ATTTGACGTGCAACACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8968
QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
Db 8969 ATTATCCACACTCTGACCATGAGCTGCAAACTGACAGCTGCTTAAAGCAGAAACAGAGA 9028
QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheThrValCysPheLeuProPheHisIleLeu 260
Db 9029 AGGCTAACCATCTGCTACTGCTTTCATTTAGTATGTTTAAACCTTCATATTCCTG 9088
QY 261 ArgValIleArgIleGluSerArgLeuSerIleSerCysSerIleGluAsnGlnIle 280
Db 9089 AGGCTCATTCGGATGGAATCTGCTGCTTTCATCAAGTGTTCATTCATTCATTCATTCATTCAT 9148
QY 281 HisGluAlaThrIleValSerArgProLeuAlaIleAlaLeuAsnThrPheGlyAsnLeu 300
Db 9149 CATGAAGCTTACATGCTTTCAGACCATTAAGCTGCTGCAACACCTTGGTAACTGTGTA 9208
QY 301 LeuThrValAlaValSerAspAsnPheGlnAlaValCysSerThrValArgCysLys 320
Db 9209 CTATATGTGTGTGTGCTGAGCAGCAAACTTTCAGCAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 9268
QY 321 ValSerGlyAsnLeuGlnAlaValLysLysIleSerTyrSerAsnAsnPro 337
Db 9269 GTAAAGGGGAACTTGGAGCAAGCAAAATAATTAAGTCAAAACCAACCT 9319

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RESULT 7

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US-09-782-974C-85
; Sequence 85, Application US/09782974C

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Publication No. US20030082534A1
GENERAL INFORMATION:
APPLICANT: Vogel, Gabriel
APPLICANT: Lind, Peter
APPLICANT: Wood, Linda S.
APPLICANT: Parodi, Luis A.
TITLE OF INVENTION: No. US20030082534A1e1 G Protein Coupled Receptor
FILE REFERENCE: 41USPHM311
CURRENT APPLICATION NUMBER: US/09/782,974C
PRIORITY FILING DATE: 2002-09-04
PRIORITY APPLICATION NUMBER: 60/165,838
PRIORITY FILING DATE: 1999-11-16
PRIORITY APPLICATION NUMBER: 09/714,449
PRIORITY FILING DATE: 2000-11-16
PRIORITY APPLICATION NUMBER: 60/198,568
PRIORITY FILING DATE: 2000-04-20
PRIORITY APPLICATION NUMBER: 60/166,071
PRIORITY FILING DATE: 1999-11-17
PRIORITY APPLICATION NUMBER: 60/166,678
PRIORITY FILING DATE: 1999-11-19
PRIORITY APPLICATION NUMBER: 60/173,396
PRIORITY FILING DATE: 1999-12-28
PRIORITY APPLICATION NUMBER: 60/184,129
PRIORITY FILING DATE: 2000-02-22
PRIORITY APPLICATION NUMBER: 60/185,421
PRIORITY FILING DATE: 2000-02-28
PRIORITY APPLICATION NUMBER: 60/185,554
PRIORITY FILING DATE: 2000-02-28
PRIORITY APPLICATION NUMBER: 60/186,530
PRIORITY FILING DATE: 2000-03-02
Remaining prior application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn version 3.1
SEQ ID NO 85
LENGTH: 1020
ORGANISM: Homo sapiens
US-09-782-974C-85

Alignment Scores:
Pred. No.: 4 27e-154 Length: 1020
Score: 1724.00 Matches: 335
Percent Similarity: 99.12% Conservative: 2
Best Local Similarity: 98.53% Mismatches: 0
Query Match: 97.35% Indels: 3
DB: 9 Gaps: 0

US-10-023-775b-2 (1-337) x US-09-782-974C-85 (1-1020)
QY 1 MetasngluProleuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAlaAla 20
DB 4 ATGAATGAGGACCTAGACCTATTGACAAATGCTTCGATTCCCGCATTTGACAGCGCT 63
QY 21 PheGlyAsnGlyThrAspGluAsnIleProleuLysMetHisTyrLeuProValIleTyr 40
DB 64 TTTGGAAATGCACTGTGTAACCACTCCACTCAAGATGCACTACCTCCCTGTTATTAT 123
QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValAlaIleSerThrTyrIlePhe 60
DB 124 GGCATTAATCTTCTCGTGGGATTTCCAGGCAATGCACTATGATATCATTACATTTTC 183
QY 61 LysMetArgProTrrPlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
DB 184 AAATAGAGACCTTGGAAAGACAGACACATCATATGCTGAACCTGGCTGCACAGATCTG 243
QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTrrPle 100
DB 244 CTGTATCTGACCGACCTCCCTCCCTGATTCACCTACTATCCAGTGGCGAAACTGGATC 303
QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
DB 304 TTTCGAGATTTCATGATGATTAATCCGCTTCAGCTTCATTCATTCATTCATTCATTCAT 363
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QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPrometSer 140
DB 364 ATCCCTTCTCTACACCGTTCACACATCTCCGCTACTGTGTATCATTCACCAATAGAG 423
QY 141 CysPheSerIleHisTyrThrArgCysAlaValAlaCysAlaValAlaTrrPleIle 160
DB 424 TGCTTTTCATTCACAAACTCGATGTCAGTGTGCTGCTGTGTGTGTGTGTGTGTGTGT 483
QY 161 SerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
DB 484 TCACGTGTACCTGTATCCGATGACCTCTCTGTATCATCAACCAAGACCAACAGAGA 543
QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrrPlyAsnLeu 200
DB 544 TCAGCTGTCTGACCTTCACCACTTCGGATGAGACTCAATACATTTAAGTGGTACACCTG 603
QY 201 IleLeuThrAlaThrPheCysLeuProLeuValIleValThrLeuGlyTyrThrThr 220
DB 604 ATTTGACCTGCAAGTACTTCTGCTCCCTGCTGTGTATGTATGTACACTTGTCTATAC 663
QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnTyrAlaArg 240
DB 664 ATTAATCACACTTTCAGCCATGAGACTGCAGCAAGCTGCTTAAAGCAGAAAGACAGA 723
QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
DB 724 AGGCTAACCACTTGTGCTACTCTTGCATTTAGATGTTTATACCTTCATACCTTG 783
QY 261 ArgValIleArgIleGluSerArg-LeuLeuSerIleSerCysSerIleGluAsnGln 280
DB 784 AGGCTAATTCAGATGCAATCTCAGCTGCTTTCATCACTTGTTCATTCAGCAATTCAGA 843
QY 280 LeHisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeu 299
DB 844 TCCATGAGCTTTCATACCTGTTTACAGCATTAATGCTGCTGTGAACCTTGGTAACTG 963
QY 300 LeuLeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCys 319
DB 904 TTACTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 963
QY 320 LysValSerIleLysLeuGlnGlnAlaValLysIleSerTyrSerAsnAsnPro 337
DB 964 AAAGTAGCGGGAACCTTGAGCAAGCAAAATAATTAATTAATCAACCAACCTT 1017

RESULT 8
US-09-943-798-1
Sequence 1, Application US/09943798
Patent No. US20020065215A1
GENERAL INFORMATION:
APPLICANT: Glaxo Group Limited
TITLE OF INVENTION: Polypeptide
FILE REFERENCE: 061021
CURRENT APPLICATION NUMBER: US/09/943,798
PRIORITY FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 831
TYPE: DNA
ORGANISM: Homo sapiens
US-09-943-798-1

Alignment Scores:
Pred. No.: 1 03e-127 Length: 831
Score: 1444.00 Matches: 276
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 81.54% Indels: 0
DB: 10 Gaps: 0

US-10-023-775b-2 (1-337) x US-09-943-798-1 (1-831)
QY 62 MetArgProTrrPlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 81
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Db 1 ATGAGACCTGGAGAGCAGCAGCATATTATGCGAAGCTGGCCGACAGATCTGCTG 60
QY 82 TTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 101
Db 61 TATGTCAGCAGCTCCCTCTCTGATTCATCTACTATGCGAGGGAACGAGATCTT 120
QY 102 GYAAPPPhemeCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerIle 121
Db 121 GGAGATTTCATGTGTAAGTTATCCGCTTACCTTCACCTTCATTCACCTGATAGCAGATC 180
QY 122 LeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPrometSerCys 141
Db 181 CTCTTCCTACCTGTTTTCAGCATCTCCGCTACTGCTGATGATTCATTCACCAATGAGCTGC 240
QY 142 PheSerIleHisLysThrArgCysAlaValAlaIaCysAlaValAlaIleIleSer 161
Db 241 TTTTCCATTACAAAACCTCGATGTGATGTGATGTGATGTGATGTGATGTGATGTGAT 300
QY 162 LeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArgThrAsnArgSer 181
Db 301 CTGTAAGCTGTATTCCTGATGACCTTTTGTATCATCATCAACCAAGGACCAAGCATGA 360
QY 182 AlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTyrAsnLeuIle 201
Db 361 GCGTGTCTGACCTCAGCAGCTCGGATGTAACATCAATCAATCAATCAATCAATCAAT 420
QY 202 LeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrIle 221
Db 421 TTGACTGTGAACTACTTCTTCTCTCCCTTGTGATGATGATGATGATGATGATGATGAT 480
QY 222 IleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArgArg 241
Db 481 ATCCACACTCTGACCCATGAGTGTGCAAACTGACAGCTGCTTAAAGCAGAAACAGAGAG 540
QY 242 LeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeuArg 261
Db 541 CTAAACCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
QY 262 ValIleArgGlyLeuSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIleHis 281
Db 601 GCATTTCCGATTCGATTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
QY 282 GluAlaTyrIleValSerArgProLeuAlaIleAlaLeuAsnThrPheGlyAsnLeuLeu 301
Db 661 GAAGCTTACATCGTTCTAGACCATTAAGCTGCTGCAACCTTGGTGAACCTGTACTA 720
QY 302 TyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLysVal 321
Db 721 TATGTGATGTGATGAGGAGACATTTTCAGCAGGCTGTCTCTCAACAGTAGAGTGAAGTA 780
QY 322 SerGlyAsnLeuGlnGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
Db 781 AGCGGAGACCTTGACCAAGCAAAAGAAATTAAGTACTCAAAACCAACCT 828

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RESULT 9
US-09-728-422-1

; Sequence 1, Application US/09728422
; Patent No. US20020128187A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehman, Tom
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20020128187A1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 787CIP2F

```

; CURRENT APPLICATION NUMBER: US/09/728,422
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/560, 875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496, 914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: pL_FL_genes Version 2.0
; SEQ ID NO: 1
; LENGTH: 1313
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (547)..(1239)
US-09-728-422-1

Alignment Scores:
Pred. No.: 7,52e-112 Length: 1313
Score: 1279,50 Matches: 246
Percent Similarity: 99,60% Conservative: 0
Best Local Similarity: 99,60% Mismatches: 1
Query Match: 72,25% Indels: 1
DB: Gaps: 0

US-10-023-775B-2 (1-337) x US-09-728-422-1 (1-1313)

QY 1 MetAsnGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
Db 547 ATGATGAGCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
QY 21 PheGlyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrLeuProAlaIleTyr 40
Db 607 TTGGAAATGTGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValAlaIleSerThrTyrIlePhe 60
Db 667 GGCATTATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
QY 61 LysMetArgProTyrPlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
Db 727 AAAATGAGACCTTGGAGAGAGCAGCAGCATCATTAATGCTGACCTGCGCAGATCTG 786
QY 81 LeuTyrIleThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyLysAsnTrpIle 100
Db 787 CTGATCTGACAGCCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 846
QY 101 PheGlyAspPheCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
Db 847 TTGGAGATTTCATGTGTAAGTTATCCGCTTACCTTCACCTTCATTCACCTGATAGCAGC 906
QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPrometSer 140
Db 907 ATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 966
QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaIaCysAlaValAlaIleIleSer 160
Db 967 TGCCTTTCATTCACAAAACCTCGATGTGATGTGATGTGATGTGATGTGATGTGATGT 1026
QY 161 SerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
Db 1027 TCACGTGATGCTGTATTCCTGATGACCTTTTGTATCATCATCAACCAAGGACCAAGCA 1086
QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTyrAsnLeu 200
Db 1087 TCAGCTGTCTGACCTCAGCAGCTCGGATGTAACATCAATCAATCAATCAATCAATCAAT 1146
QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
Db 1147 ATTTGACTGTGAACTACTT--TGCTCTCTCTGATGATGATGATGATGATGATGATGAT 1204
QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240

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OY      167  PromethrPheulelethserThrsnaqrThrsanaygSerAlaCysLeuAspLeu 186
Db      286  CGATAGACTCTTCTTGATCATCAACAACAAGGACCAACAATACAGCTGTCTGACCCTC 227
OY      187  ThrSerAspLeuAsnThrIleuStrpYrAsnLeuIleuThrAlaThrThr 206
Db      226  ACAGTTCGGATGAATCAATCAACTTAAAGTGTCAACAACGTGATTTGACGCAACTACT 167
OY      207  PheCysLeuProLeuValIleValThrLeuCysTyrThrThrIleIleHisThrLeuThr 226
Db      166  TTCTGCCTCCCTTGGTGTGATGAGTACACTTTCGCTATACACAGATTAATACACTGTGACC 107
OY      227  HisGlyLeuGlnThrTrpSerCysLeuGlnGlyAlaGlyLeuThrIleLeuLeu 246
Db      106  CATTGACCTGCAAACTGACAGCTGCTTAAGCAAGAAAGCAGCAAGGCTAAACCATTCGCTA 47
OY      247  LeuLeuAlaPheTyrValCysPheLeuProPhe 257
Db      46  CTCCTTGCAATTTTACGTATGTTTATTTACCCTTC 14

RESULT 12
US-09-077-173A-1
: Sequence 1, Application US/09077173A
: Publication NO. US20030082674A1
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: RECEPTOR AND NUCLEIC ACID MOLECULE ENCODING
: TITLE OF INVENTION: SAID RECEPTOR
: NUMBER OF SEQUENCES: 4
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/077,173A
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/BE 96/00123
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1429 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 181..1275
: US-09-077-173A-1

Alignment Scores:
Pred. No.: 2,56e-39 Length: 1429
Score: 514.00 Matches: 101
Percent Similarity: 57.29% Conservative: 64
Best Local Similarity: 35.07% Mismatches: 119
Query Match: 29.02% Indels: 4
DB: 9 Gaps: 2

US-10-023-775B-2 (1-337) x US-09-077-173A-1 (1-1429)
OY      26  AspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyrGlyIleIlePheLeu 45
Db      268  GATGAGAGAT-----TTCAAGTTTCATCTCGTCGCTGTGACTATGACGTATGCTTTGTG 321
OY      46  ValGlyPheProGlyAsnAlaValIleSerThrTyrIlePheLysMetArgProTrp 65
Db      322  CTGGGCTTGGGCTTAAACGCCCAACCCCTATGGCTCTTCATCTTCGCGCTCCGACCTGG 381
OY      66  LysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeuLeuTyrLeuThrSer 85
Db      382  GATGCAACGGCCACCTACTATGTTCCACCTGGGCAATGTGAGACACCTGTATGTCTGTG 441

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Oy		86	LeuPnropheuleuIIeHISTYrTYAlSerSeriylguIsntPrIlePhelGlyAspPheket	105
Dd		442	CTGGCCACCACATCTACTATTATAGCAACCCACAACAACATGCGCCCTTTGGCAGTAGATC	501
Oy		106	CysLysPheIIeaAgPheSerPheHisPheasInLeutySerSeriIeLeuPheLeuthr	125
Dd		502	TGCAAGTTCGRCGGCTCTTTCTGTATAGGAACCGTACGACAGTGCTTTCTTCAC	561
Oy		126	CysPheSerIIePheaGTyrCysValIIeiIleHisProMetSerGysPheSeriIleis	145
Dd		562	TGCATCACCGCGACACCGCTTACCTGGCATTCGCCAACCCACCACTTCGGGCATCAGCTGGGGC	621
Oy		146	LysThrArgCysAlaValAlaCysAlaValValTrpIleIleSerLeuValAlaVal	165
Dd		622	GCGCCCTGGCCCGCAGAGCCCTTCTGCTGCCGTGACATTGGTTGGTCGTAAGCGGCTGCTC	681
Oy		166	IleProMetThrPheLeuIleThrSerThraAnaGrThraAnaArgSerAlaCysLeuasp	185
Dd		682	GTGCCAACAACGTTCTTTGTCACAAACCGACAAGAAGGACACCGCTGCTGCATGAC	741
Oy		186	LeuThrSerSeraspGlueAsnThrIleLystrIryrAnLeuIIeLeuThAlaThr	205
Dd		742	ACCACTCGGCCCTGAAGAGTTGGACCACTATGTGCACTTCACCTCGCGGCTATGGGGCTG	801
Oy		206	ThrPheCysLeuProLeuValIIeValThrLeuCysTryThrThrIleIIeHisThrLeu	225
Dd		802	CTCTTTGGCGGCCCTGCGTGGTCACGTCTTTGGCTATGAGACATAGCGCTGCGCGCTG	861
Oy		226	ThriIslgIleU-----GIlnThrasPserCysLeuLysGlnLysAlaArgrLeuthr	243
Dd		862	TATCAGCCCTTGTCCAGAGCTGCACAGTGGCTTCTGCGCCGCTCTCTCCGACCATTA	921
Oy		244	IleLeuLeuLeuAlaAlphaPetyrValCysPheLeuProPheHisIleLeuArValIle	263
Dd		922	GCTGTGGTGGCTAGCTGCTTTGGTGTGTGTGCTTCCGCTTTCACATCACCAGCACTT	981
Oy		264	ArgIleGuSerArgrLeuSerIleserCysSerIleGuasnGlnIIeHisGUAla	283
Dd		982	TACTACCTGGCGACGCTGTTGGAGAGCTGACGCGGACAGTACGAACTGTCAACGTGCTC	1041
Oy		284	TyrIleValSerArgrProLeuAlaAlaLeuasnThrPheGlyAsnLeuLeuTyrrAl	303
Dd		1042	TATAAAGTACGTGGCCCCCTGGCCAGTGCACAACAGTGCCTGGATCCTGTGCTTACTTG	1101
Oy		304	ValValSerAspAsnPheGlnGln	311
Dd		1102	CTCAGTGGGACAAATATCGACGT	1125
RESULT 13				
US-10-270-587-1				
; Sequence 1, Application US/10270587				
; Publication No. US20030054487A1				
; GENERAL INFORMATION:				
; APPLICANT: Li, Yi				
; TITLE OF INVENTION: Human G-Protein Coupled Receptor				
; FILE REFERENCE: PFI21/C2				
; CURRENT APPLICATION NUMBER: US/10/270, 587				
; PRIOR FILING DATE: 2002-10-16				
; PRIOR APPLICATION NUMBER: US 09/908, 593				
; PRIOR FILING DATE: 2001-07-20				
; PRIOR APPLICATION NUMBER: US 08/781, 456				
; PRIOR FILING DATE: 1997-01-10				
; PRIOR APPLICATION NUMBER: US 60/009, 902				
; PRIOR FILING DATE: 1996-01-11				
; NUMBER OF SEQ ID NOS: 9				
; SOFTWARE: Patent version 3.1				
SEQ ID NO 1				
LENGTH: 1428				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-10-270-587-1				

Alignment Scores:

Pred. No.: 7.42e-37 Length: 1428
Score: 488.00 Matches: 111
Percent Similarity: 56.21% Conservative: 61
Best Local Similarity: 36.27% Mismatches: 122
Query Match: 27.56% Indels: 12
DB: 9 Gaps: 6

US-10-023-775b-2 (1-337) x US-10-270-587-1 (1-1428)

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QY 23 AsnCysThrAspGluAsn-----IleProLeuLysMetHisTyrLeuPro 37
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Db 113 AATGCAACTGCCAAATGCTGCGACAGAGGCTCCCTGGAAAGTACTACTCTCC 172
QY 38 ValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThr 57
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 173 ATTTTATGGAGATGAGTTCGTTGTGGAGTCTTGAAATACATGTTGTTACGGC 232
QY 58 TyrIlePheLysMetArgProTrrPlySerSerThrIleIleMetLeuAsnLeuAlaCys 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 TACATCTCTCTCTGAGAGAACTGGACAGCATATATTTATCTTAACTCTCTGTC 292
QY 78 ThrAspLeuTyrIleThrSerIleHisTyrArgCysAlaValAlaCysAlaVal 97
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 293 TCTGACTTACTTCTTCTGTCACCTCCCATGCTGATTAAGAGATTATGCCAATGGA 349
QY 98 AsnTrrIlePheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeu 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 350 AACGATATATGAGACGCTGCTGCATTAAGCAACGATATGCTTCATGCCAACCTC 409
QY 118 TyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgGlyCysValIleIleHis 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 410 TATACCGACATCTCTCTTCTCATTATGACATATGATCTGATATATTAAGTAT 469
QY 138 PrometSerCysPheSerIleHisTyrArgCysAlaValAlaCysAlaVal 157
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 470 CTTTCCGAGAACCTTCTGCAAAAGAGAGTGTCTATTTAACTCCCTGGCCATG 529
QY 158 TrrIleIleSerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArg 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 530 TGGGTTTATTAACCTTAGATGATTAACCATTAATCTCCCTTAAATTCGTATTA 589
QY 178 ThrAsnArgSerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrr 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 590 GACAAATGGCACACCTTAATGATTTGCAAGTTCTGAGACCCCACTCAACCTCAT 649
QY 198 TyrAsnLeuIleThrAlaThrThrPheCysLeuProLeuValIleAlaThrLeuCys 217
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 650 TACAGCATGTCTTAACACAGCTTGGGTTCTTCTTCTCTTTTGTGATGTGTTCTT 709
QY 218 TyrThrThrIle--IleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLys 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 710 TATTTACAAATGCTCTCTTCTTAACAGAGAAATGAGAGTTGCTTACTGCTGCC 769
QY 237 ---GlnLysAlaArgAlaGlyLeuThrIleLeuLeuLeuAlaPheTrrValCysPheLeu 255
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 770 CTTGAAAGGCTCTCAACTTGGTGCATGAGCATGCAATCTTCTGCTTGTACCA 829
QY 256 ProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSer-----Ile 272
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 830 CCTATATACGTATGCGGAATGTGAGATGCTTACGCTGGGAGATTGGAGCACTAT 889
QY 273 SerCysSerIleGluAsnGlnIleHisGlyAlaTrrIleValSerArgProLeuAlaVal 292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 890 CAGTGCAGCT---CAGGTCTGATCACTCACTCTTTTACTTGTGACAGGCTGTGCTTT 946
QY 293 LeuAsnThrPheGlyAsnLeuLeuTrrValValAlaValSerAspAsnPheGlnAlaVal 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 947 CTGACAGGTGTCAATCAACCTGCTTCTATTTCTTGTGGAGATCACTTACAGGACATG 1006
QY 313 ValCysSerThrValArg 318
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Db 1007 CTGATGATCACTGAGA 1024
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RESULT 14

US-09-826-791-1

: Sequence 1, Application US/09826791

: Patent No. US20010039037A1

: GENERAL INFORMATION:

: APPLICANT: Pfizer Inc

: TITLE OF INVENTION: No. US20010039037A1el Polypeptide

: FILE REFERENCE: PC10914ADAM

: CURRENT APPLICATION NUMBER: US/09/826,791

: PRIOR FILING DATE: 2001-04-05

: PRIOR APPLICATION NUMBER: 0008504.3

: PRIOR FILING DATE: 2000-04-05

: PRIOR APPLICATION NUMBER: 60/198,367

: NUMBER OF SEQ ID NOS: 6

: SOFTWARE: PatentIn Ver. 2.0

: SEQ ID NO 1

: LENGTH: 993

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-826-791-1

Alignment Scores:

Pred. No.: 4.89e-37 Length: 993
Score: 487.50 Matches: 111
Percent Similarity: 55.03% Conservative: 64
Best Local Similarity: 34.91% Mismatches: 114
Query Match: 27.53% Indels: 29
DB: 10 Gaps: 10

US-10-023-775b-2 (1-337) x US-09-826-791-1 (1-993)

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Db 40 AACTGCAATGGAAC-----TTCAAGAGAAATTTTCCCAATGATATATCTGATA 93
QY 43 IlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTrrIlePheLysMet 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 94 ATATTTTCTGGGAGAGCTTGGGAATAGG-----TTGTCATATATGTTTTC---CTG 144
QY 63 ArgProTrrPlySerSerThr-----IleIleMetLeuAsnLeuAlaCysThrAsp 79
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 145 CAGCTTATTAAGAGTCAATCATCTGTAACGTTTCTGCTAATATGCGCAATTTCAGAT 204
QY 80 LeuLeuTrrLeuThrSerLeuProPheLeuIleHisTyrTrrAlaSerGlyLysAsnTrr 99
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 205 CTCTGTTCATTAACACGCTTCCCTTCAAGGCTGACTATATATCTTACAGGCTCAATTGG 264
QY 100 IlePheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTrrSer 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 265 ATATTTGAGACACCTGGCTGACAGATTAATGCTTATTCCTGTATGTCACACATGACAGC 324
QY 120 SerIleLeuPheLeuThrCysPheSerIlePheArgGlyCysValIleIleHisPromet 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 325 AGTATTTATTTCTGACCGCTGAGCTGAGTGTGCTGCTGCAATAGGTTCCCTTT 384
QY 140 SerCysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTrrPile 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 385 CCGCTTTCATGATGACACAGATCAGAGAGTCCCTGATCTCTGTGGATCATATGATC 444
QY 160 IleSerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArgThrAsn 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 CTATATATGAGCTTCCCTCAATA-----ATGCTCTGACAGATGCTCTGAGACAGAAC 495
QY 180 ArgSerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLys----- 196
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 GGCAGT-----GTCAATCATGCTTATGAGAGCTGATCTTATTAATATGCTTAAG 543
QY 197 -----TrrTyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeuValIleVal 214
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 544 CTGACAGCACTGAATCATATATGCTTGTGTGGTGGCTGCTGCTGCTATTTTTCACACTC 603
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QY 215 ThrLeuCySerThrThrIleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCys 234
DB 604 AGCATCTGTATCTCTGTATCATTCATTCGGGTTCTGTAAAAGTGAGAGTCCCAAAATCGGGG 663
QY 235 LeuLys-----GlnLysAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyr 251
DB 664 CTGGGGGTTTTCACAGAGAGGAGGAGTACACCATCATCATCATCTGTATCATCTCTTC 723
QY 252 ValCysPheLeuProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSer 271
DB 724 TTGTGTTTCTCTCCATCATCATCATCTGTATCATCTGTATCATCTGTATCATCTGTAT 783
QY 272 IleSerCysSerIleGlnLysGlnIleHisGlnAlaTyrIleValSerArgProLeuAla 291
DB 784 TTA-----TGCAGAGAGAGGAGTGCATTAAGCTTTGGTATATCATCTGTATCATCT 834
QY 292 AlaLeuAsnThrPheGlyAsnLeuLeuLeuTyrValIleValSerAspAsnHeuGlnGln 311
DB 835 GCAGGCAATGCTGCTCATATCTCTGTATCATCTGTATCATCTGTATCATCTGTATCAT 894
QY 312 AlaValCysSerThrValArgCysLysValSerGlyAsnLeuGlnAlaLys 329
DB 895 AGACTAAAGTCTGCATCTAGA-----AAAGGCAATCCACAGAGAGCAAG 939

RESULT 15
US-09-828-478-1
; Sequence 1, Application US/09828478
; Patent No. US20020155528A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/09/828,478
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-828-478-1

Alignment Scores:
Pred. No.: 5,24e-37 Length: 1041
Score: 487.50 Matches: 111
Percent Similarity: 55.03% Conservative: 64
Best Local Similarity: 34.91% Mismatches: 114
Query Match: 27.53% Indels: 29
DB: 9 Gaps: 10

US-10-023-775b-2 (1-337) x US-09-828-478-1 (1-1041)
QY 23 AsnCysThrAspGlnAsnIleProLeuLysMetHisTyrLeuProValIleTyrGlyIle 42
DB 88 AACTGCACAAATTTGAAAC-----TTCAAGAGAGAAATTTTCCCAATGTATATCTGATA 141
QY 43 IlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePheLysMet 62
DB 142 AATATTTTCTGGGGAGTCTTGGGAAATGG-----TTGTCATATATATGTTTC--CTG 192
QY 63 ArgProTyrPheSerSerThr-----IleIleMetLeuAsnLeuAlaCysThrAsp 79
DB 193 CAGCCTTAAAGAAATGCAATCTGTGAAGCTTTTCATGCTTAATCTGCCCATTTTCAGAT 252
QY 80 LeuLeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyLysAsnTyr 99
DB 253 CTCCTGTTTCATTAAGACAGCTCTCCCTTCAAGGAGCTGATATATCTTAAGAGCTCAATGG 312

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QY 100 IlePheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSer 119
DB 313 AATATTTGGAGAGCTGGCTGCAGAGATATGCTTATCTTGTATGTAACATGTRACAC 372
QY 120 SerIleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPhe 139
DB 373 AGTATTTATTTCTCTGACCGCTGAGATGTTGGCGTTCTTCCGCAATGTTACACCTTT 432
QY 140 SerCysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValTyrPhe 159
DB 433 CGGCTTCTGCATGTCACAGATATGCTGCTGTATCTGTGAGATATGAGATC 492
QY 160 IleSerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsn 179
DB 493 CTATCATGCTTCTCCCAAT-----ATGCTCTGAGACAGTGGCTCTGAGCAGAAC 543
QY 180 ArgSerAlaCysLeuAspLeuThrSerSerAspGlnLeuAsnThrIleLys----- 196
DB 544 GGCAGT-----CTCACATCATGCTTAGAGCTGAATCTGTATTAATTTGCTAAG 591
QY 197 -----TPTTyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeuValIleVal 214
DB 592 CTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 651
QY 215 ThrLeuCySerThrThrIleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCys 234
DB 652 AGCATCTGTATCTCTGTATCATTCATTCGGGTTCTGTAAAAGTGAGAGTCCCAAAATCGGGG 711
QY 235 LeuLys-----GlnLysAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyr 251
DB 712 CTGGGGGTTTTCACAGAGAGGAGGAGTACACCATCATCATCATCTGTATCATCTCTTC 771
QY 252 ValCysPheLeuProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSer 271
DB 772 TTGTGTTTCTCTCCATCATCATCATCTGTATCATCTGTATCATCTGTATCATCTGTAT 831
QY 272 IleSerCysSerIleGlnLysGlnIleHisGlnAlaTyrIleValSerArgProLeuAla 291
DB 832 TTA-----TGCAGAGAGAGGAGTGCATTAAGCTTTGGTATATCATCTGTATCATCT 882
QY 292 AlaLeuAsnThrPheGlyAsnLeuLeuLeuTyrValIleValSerAspAsnHeuGlnGln 311
DB 883 GCAGGCAATGCTGCTCATATCTCTGTATCATCTGTATCATCTGTATCATCTGTATCAT 942
QY 312 AlaValCysSerThrValArgCysLysValSerGlyAsnLeuGlnAlaLys 329
DB 943 AGACTAAAGTCTGCATCTAGA-----AAAGGCAATCCACAGAGAGCAAG 987

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: May 29, 2003, 22:24:09 ; Search time 295 Seconds
(without alignments)
2572.622 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1771	100.0	1011	24 AAL43942	Human G protein-co
2	1771	100.0	1014	22 AAS07948	Human G-protein co
3	1771	100.0	1014	24 AB078847	Human G-protein co
4	1771	100.0	1014	24 ABN85630	Human P2Y-1-like rec
5	1771	100.0	1014	24 AD34278	Human AXOR89 (G-pr
6	1771	100.0	1014	24 ABK11381	Human DNA encoding
7	1771	100.0	1014	24 AAK98323	Human purinergic-r
8	1771	100.0	1014	24 AAD26370	Human G-protein co
9	1771	100.0	1288	24 AB156197	Human P2Y-11 enco
10	1771	100.0	5435	24 AB156198	Human P2Y-11 enco
11	1771	100.0	9905	24 AAK98324	Human purinergic-r
12	1764	99.6	1729	22 AAS08362	Human cDNA encodin
13	1764	99.6	1729	23 ABY24026	Human prostrate exp
14	1764	99.6	1729	23 ABY25767	Human prostrate exp
15	1764	99.6	1729	23 ABY29909	Human prostrate exp
16	1764	99.6	1729	23 ABY30024	Human prostrate exp
17	1724	97.3	1020	22 AAK91011	Human nGPCR54 codi
18	1444	81.5	831	24 ABN85629	Human P2Y-1-like rec
19	1279.5	72.2	1313	22 AAK52430	Human polynucleoti
20	993	56.1	740	23 ABY15662	Human prostrate exp
21	940	53.1	578	22 AAK50998	Human nGPCR54 codi
22	861.5	48.6	545	22 ABA08326	Human P2Y purinoco
23	861.5	48.6	545	22 AAK53414	Human polynucleoti
24	751	42.4	539	23 ABY39127	Human prostrate exp
25	751	42.4	539	23 ABY45465	Human prostrate exp
26	623	35.2	478	23 ABY15479	Human prostrate exp
27	617	34.8	426	23 ABY36271	Human prostrate exp
28	617	34.8	426	23 ABY45310	Human prostrate exp
29	597	33.7	2245	24 ABK11380	Human P2Y-1-like G
30	595	33.6	435	23 AAV06310	Human prostrate exp
31	567	32.0	6721	24 AAS18599	Purinergic recepto
32	567	32.0	6721	24 AAS18600	Purinergic recepto
33	550	31.1	442	23 ABY08973	Human prostrate exp
34	514	29.0	1429	18 AAT74321	Human P2Y4 recepto
35	492	27.8	1428	18 AAT75116	Human ATP receptor
36	491.5	27.8	1041	22 AAT50800	Human cDNA encodin
37	487.5	27.5	993	24 AAT77276	Human G-protein co
38	487.5	27.5	1026	24 AAS98140	Human DNA for pote
39	487.5	27.5	1039	22 AAS10778	DNA encoding cyste
40	487.5	27.5	1041	22 AAT26608	Human P2Y-1-like GPC
41	487.5	27.5	1041	22 AAS07941	Human cDNA encodin
42	487.5	27.5	1041	24 AAD28591	Human CysLT2 GPCR
43	487.5	27.5	1041	24 AAT77279	Human G-protein co
44	487.5	27.5	1260	22 AAD13709	Human G-protein co
45	487.5	27.5	1430	22 AAT26609	Human P2Y-1-like GPC

ALIGNMENTS

RESULT 1
ID AAL43942 standard; DNA: 1011 BP.
ID AAL43942:

AC AAL43942:
XX
XX
DT 27-SEP-2002 (first entry)

DE Human G protein-coupled receptor coding sequence.

XX Human; gene therapy; G protein-coupled receptor; drug development;
KW central nervous system disease; endocrine disease; metabolic disease;
KW cancer; respiratory disease; digestive disease; immune disease;
KW inflammation; infection; circulatory disease; gene; ds.

OS Homo sapiens.
XX
XX Key Location/Qualifiers

FT CDS 1..1011
 FT /*tag- a
 FT /partial
 FT /product= "Human G-protein coupled receptor"
 FT /note= "No stop codon is given"
 XX
 XX WO200257441-A1.
 XX
 XX 25-JUL-2002.
 XX
 XX 17-JAN-2002; 2002WO-JP00270.
 XX
 XX 18-JAN-2001; 2001JP-0010714.
 XX 30-MAR-2001; 2001JP-0102484.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX
 XX Miwa M, Ito T, Shintani Y, Miyajima N;
 XX WPI; 2002-566800/60.
 XX P-PSDB; AAO15399.
 XX
 XX Human kidney-originated G protein-coupled receptor protein TGR30 and
 XX encoded DNA, for developing drugs to treat central nervous diseases,
 XX endocrine diseases, metabolic diseases and cancer, including gene
 XX therapy -
 XX
 XX Claim 6; Page 90-91; 98pp; Japanese.
 XX
 XX The invention comprises the amino acid and coding sequence of a human G
 XX protein-coupled receptor. The DNA and protein sequences of the invention
 XX are useful for developing drugs to prevent or treat (gene therapy):
 XX central nervous system diseases; endocrine diseases; metabolic diseases;
 XX cancer; respiratory diseases; digestive diseases; immune diseases;
 XX inflammations; infections; and circulatory diseases. The present DNA
 XX sequence encodes the human G protein-coupled receptor of the invention.
 XX
 XX Sequence 1011 BP; 257 A; 263 C; 188 G; 303 T; 0 other:
 XX
 XX Alignment Scores:
 XX Pred. No.: 4.95e-145 Length: 1011
 XX Score: 1771.00 Matches: 337
 XX Percent Similarity: 100.00% Conservative: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX DB: 24 Gaps: 0
 XX
 XX US-10-023-775B-2 (1-337) x AAI43942 (1-1011)
 QY 1 MetasnGLuProlEuAsPTyRLeuAlaAsnAlaSerAspPheProAspTyRAlaAla 20
 Db 1 ATGATATGAGCCACATGACTATTTAGCAAAATGCTTCTGATTTCCCGATATGAGCTGCT 60
 QY 21 PheGlyAsnCySThrAspGluAsnIleProLeuLysMetHisTyRLeuProValIleTyr 40
 Db 61 TTtGGAAATTCACATGATGAAACATCCCACTCAAGATGACCTACCTCCGTTATTTAT 120
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 Db 121 GGCATATATCTCTCGTGGGATTTCCAGCAATGCAGATGATGATCCACTTACATTTC 180
 QY 61 LysMetLArgProTrrPlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 Db 181 AAAATGAGACCTTGGAAGAGCAGCACCATCATATGCTGGAACCTGGCCTGCAGACATCTG 240
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyRAlaSerGlyGluAsnTrrPle 100
 Db 241 CTGATCTGACACCTCCCTCTCTCTATTTACTACTATGCGCACTGGGAAACTGGATTC 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 Db 301 TTtGGAATTTTCATGATGATTAATCCGCTTACGCTTCATTTCAACCTGTATAGCAGC 360

QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyRcysValIleIleHisPrometSer 140
 Db 361 ATCCCTCTCCACCTGCTTTTACATCTTCGCTACTCTGTGATCATTCACCAATCAGC 420
 QY 141 CysPheSerIleHisTyRArgCysAlaValAlaCysAlaValAlaTrrIleIle 160
 Db 421 TGCCTTTCATTCACAAACCTGACATGTCAGCTTGTAGCTGCTGCTGTGTGATCATTT 480
 QY 161 SerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 Db 481 TCACCTGTAGCTGTGATTCGATGACCTCTCTTGTATCATATACCAACAGCAGCA 540
 QY 541 TCAGCTGTCTGACACTCACAGTTCGATGACCTCAATTAATTAAGTGTACAACTG 600
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThr 220
 Db 601 ATTTGACTGCACTACTTCTGCTCCCTGCTGTGATGACGACCTTGTATATACAG 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 Db 661 ATTATCCACACTCTGACCCATGACACTGCAAACTGACAGCTGCTTAAGCAAAAGCAG 720
 QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyRValCysPheLeuProPheHisIleLeu 260
 Db 721 AGGCTAACCATTCCTGCTACTCTCTGATTTAGCTATGTTTATACCTTCATATCTTG 780
 QY 261 ArgValIleArgIleGlnSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 Db 781 AGGCTCATTCGATGCAATTCGCTGCTTTCATATCATGTTTCCATTTAGAAATCAGATC 840
 QY 281 HisGluAlaTyRILEValSerArgProLeuAlaIleLeuAsnThrPheGlyAsnLeuLeu 300
 Db 841 CATGAGCTTTCATGCTTTTACAGCACTTACTCTCTGACACCTTGTGTAACCTGTA 900
 QY 301 LeuTyRValValIleSerAspAsnPheGlnAlaValCysSerThrValArgCysLys 320
 Db 901 CTATATGCTGCTGCTCAGCAGCACTTCAGCAGCTGCTGCTCAACAGTATGATGCAAA 960
 QY 321 ValSerGlyAsnLeuGlnAlaLysLysIleSerTyRAsnAsnPro 337
 Db 961 GTAAAGCGGAACTTGAGCAAGCAAAAGAAATATGATTAATCAAAACACCT 1011
 RESULT 2
 ID AAS07948 standard; cDNA: 1014 BP.
 AC AAS07948;
 AC 23-OCT-2001 (first entry)
 DE Human cDNA encoding G-protein coupled receptor, hRUP21.
 KW Human; G-protein coupled receptor; GPCR; hRUP21; agonist;
 KW Inverse agonist; lung cancer; ss.
 XX Homo sapiens.
 OS
 XX
 XX Key location/Qualifiers
 FT CDS 1..1014
 FT /*tag- a
 FT /product= "hRUP21"
 PN WO200136471-A2.
 XX 25-MAR-2001.
 PD 16-NOV-2000; 2000WO-US31509.
 PF 17-NOV-1999; 99US-0166088.
 PR 17-NOV-1999; 99US-0166099.
 PR 17-NOV-1999; 99US-0166369.

PR 23-DEC-1999; 9905-0171900.
 PR 23-DEC-1999; 9905-0171901.
 PR 23-DEC-1999; 9905-0171902.
 PR 11-FEB-2000; 2000US-0181749.
 PR 14-MAR-2000; 2000US-0189258.
 PR 14-MAR-2000; 2000US-0189259.
 PR 10-APR-2000; 2000US-0195898.
 PR 10-APR-2000; 2000US-0195899.
 PR 10-APR-2000; 2000US-0196078.
 PR 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0203630.
 PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.

XX (AREN-) ARENA PHARM INC.

PI Chen R, Dang HT, Lowitz KP;

DR WPI: 2001-355616/37.

XX P-PSDB: AAU04375.

PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -

XX Claim 55; Page 113-114; 159pp; English.

CC The sequence encodes a human G-protein coupled receptor (GPCR),
 CC hRUR21. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system. Incorporating GPCRs can be
 CC utilized to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.

XX Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

XX Alignment Scores:

Pred. No.:

Score: 4.97e-145

Percent Similarity: 1771.00

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 22

US-10-023-775b-2 (1-337) x AAS07948 (1-1014)

OY 1 MetANGLPProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 DB 1 ATGAAATGACCCACTGACATATTAGCAAAATGCTTCGATTTCCCGCATTAAGAGCTGCT 60
 OY 21 PheGlyAsnCySThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
 DB 61 TTGGAAATTCGACAGATGAAACATCCACATCAAGATGCACTACTCCCTTTATTTAT 120
 OY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 121 GGCATTATCTCTCGTGGGATTTCCAGCAATGCGATGATATCCACTTACATTTTC 180
 OY 61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 181 AAAATGAGACCTTGGAGAGACGACCAATCATTAATGCTGAGCTGCAAGATCTG 240
 OY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyLysAsnTrpIle 100

DB 241 CTGTATCTGACAGCCTCCCTTCGATTCACACTACTATGACAGTGGCAAAACTGATC 300
 OY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 301 TTGGAGATTTATGATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 360
 OY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSer 140
 DB 361 ATCCCTTCCTCCTACCGCTTTCAGCATCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 OY 141 CysPheSerIleHisLysThrArgCysAlaValAlaIleCysAlaValAlaTrpIleIle 160
 DB 421 TCGTTTTCATTCACAAACGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
 OY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCACGTGTAGCTGTCTTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 540
 OY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTyrAsnLeu 200
 DB 541 TCAGCCTGTCTGACCTTCACAGTTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 600
 OY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 601 ATTTGACTGCAACTGCTTTCGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 OY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 661 ATTATCCACACTCTGACCCCATGACACTGACACTGACACTGACACTGACACTGACACTG 720
 OY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 721 AGCGTACCACTTCTGCTACTCTTCGATTTTACGATTTTATTTTACCTTCATATCTTG 780
 OY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 781 AGGGCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 840
 OY 281 HisGluAlaThrIleValSerArgProLeuAlaIleAlaLeuAsnThrPheGlyAsnLeu 300
 DB 841 CATGAAGCTTACATGCTTCTTCTGACCATTAAGCTGCTGACCATTAAGCTGCTGACCAT 900
 OY 301 LeuTyrValIleValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGCTGTGCTGACGCAACAATTTCAGCAGCGTGTCTGCTCAACATGATGATCAAA 960
 OY 321 ValSerGlyAsnLeuGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 961 GTAAGCGGGAACCTTGAGCAAGCAAAAGAAATTAATTAATTAATTAATTAATTAAT 1011
 RESULT 3
 ABQ78847
 ID ABQ78847 standard; cDNA; 1014 BP.
 AC ABQ78847;
 XX
 DT 04-OCT-2002. (first entry)
 XX
 DE Human G-protein coupled receptor PFI-019 cDNA.
 KW Human: G-protein coupled receptor; GPCR; PFI-019; neuroprotective;
 KW anti-inflammatory; cytoskeletal; cardiovascular; antiallergic; hypotensive;
 KW arteriosclerosis; osteopathic; hypertension; asthma;
 KW arteriosclerosis; gene; ss.
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT CDS 1..1014
 FT /tag= a
 FT /product= "PFI-019"
 XX
 PN EP1219638-A2.

XX 03-JUL-2002.
 PD 04-DEC-2001; 2001EP-0310136.
 XX 18-DEC-2000; 2000GB-0030854.
 XX 04-MAY-2001; 2001GB-0011031.
 PR (PEIZ) PFIZER LTD.
 PA (PEIZ) PFIZER INC.
 PI FIDOCK MD;
 XX WPI; 2002-521945/56.
 DR P-PSDB; ABB81902.
 XX New G-protein coupled receptor (GPCR) polypeptide with homology to p2y
 PT putinoceptor, useful for treating e.g. inflammation or cancers in a
 PT patient, or for screening GPCR agonists or antagonists for treating
 PT these diseases
 XX
 PS Claim 1; Page 12; 19pp; English.

XX The invention relates to a novel G-protein coupled receptor (GPCR), and
 CC the polynucleotide encoding it. The protein of the invention has
 CC neuroprotective, anti-inflammatory, cytosolic, cardiovascular,
 CC antiallergic, hypotensive, antihypertensive, and osteopathic
 CC activity. The GPCR polypeptide is useful for manufacturing a medicament
 CC for treating a patient who needs to upregulate a receptor. Preferably,
 CC therapeutically useful areas are hypertension, asthma, and
 CC atherosclerosis. The sequence encodes the G-protein coupled receptor
 CC of the invention, PFI-019.

XX Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Alignment Scores:

Pred. No.: 4.97e-145 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-10-023-775b-2 (1-337) x ABQ78847 (1-1014)

QY 1 MetasngluproleuaspTYrLeuAlaAsnAlaSeraspPheProAspTYrAlaAla 20
 DB 1 ATGATGAGCCACTAGACTATTAGCAATGCTTCTGATTTCCCGATTATGAGCTGCT 60
 QY 21 PheGlyAsnCystrhrAspGluAsnIleProLeuLysMetHisTYrLeuProValIleTyr 40
 DB 61 TTGGAATATGCACTGATGAAACATCCCACTCAAGATGACACTCCCTGATTATTTAT 120
 QY 41 GlVlellePheLeuValGlyPheProGlyAsnAlaValIleSerThyTyrIlePhe 60
 DB 121 GGCATTAATCTTCCGCGGGATTTCCAGGCAATCAGATGATATCCACTTACATTTTC 180
 QY 61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnAlaCysThrAspLeu 80
 DB 181 AAAATGAGACCTTGGAAAGAGAGACACATCATTTTGTGTAACCTGGCTGCACAGATCTG 240
 QY 81 LeuTYrLeuThrSerIleuProPheLeuIleHisTYrAlaSerGlyGluAsnTrpIle 100
 DB 241 CTGTATCTGACACACCTCCCTTCCTGATTCATCATATGACCACTGGGAAACTGGATC 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 301 TTGGAATATTCATGATGATTTATCCGCTTCAGCTTCCATTCAACCTGTATAGCAGC 360
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 DB 361 ATCTCTTCTCCTACCTGTTTCAGCATCTTCGCTACTGTGTGATCATTCACCAATGAGC 420

QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTrpIle 160
 DB 421 TGCTTTCCATTCCAAAACATGATGCACTTTAGCTGTGCTGGTGGATCATCAT 480
 QY 161 SerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCACGTGAGCTGTATCCGATGACCTTCTTGATCATCATCAACCAAGAGCAAGACA 540
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspLysLeuAsnTrpIleTyrTrpTyrAsnLeu 200
 DB 541 TCACCTGTCTGCACTCCACATCGATGATGATCACTCATATTAAGTGTACCAACTA 600
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValIleThrLeuCysTyrThrThr 220
 DB 601 ATTTTGACTGCACTACTTGTGCTCCCTGCTGATGATGATGATGATGATGATGATGAT 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysAlaArg 240
 DB 661 ATATTCACACACTGCACTGACCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 720
 QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 721 AGCTTAACCACTTCTGCTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 261 ArgValIleArgIleGlySerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 781 AGGCTATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 841 CATGAACCTTACATCGTTTTCAGACATTTACTCTCTCTGCAACCTTTGTTAACCTGTTA 900
 QY 301 LeuTyrValValIleSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 321 ValSerGlyAsnLeuGlnGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 961 GTAGCGGGAACCTTGAGCAAGCAAGAAATAGTTACTCAACAACACCTG 1011

RESULT 4
 ID ABB85630 standard; DNA; 1014 BP.
 AC ABB85630;
 XX 18-SEP-2002 (first entry)
 DE Human P2Y-1-like receptor variant encoding gene SEQ ID NO 3.
 XX Human; P2Y-1-like receptor; HIPHUM 0000037; immunity; inflammation;
 KW cancer; Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;
 KW immunomodulator; anti-inflammatory; cytosolic; antistatic;
 KW gastrointestinal; anti-ulcer; antirheumatic; antiallergic; virucide;
 KW antibacterial; immunosuppressive; dermatological; nephrotoxic;
 KW antiallergic; analgesic; receptor; gene; ds.
 XX Homo sapiens.
 OS
 XX
 XX
 FH key Location/Qualifiers
 FT 1..1014
 FT CDS /tag= a
 FT /product= "P2Y-1-like receptor variant"
 XX GB2369364-A.
 XX 29-MAY-2002.
 PD 31-AUG-2001; 2001GB-0021215.
 PF 01-SEP-2000; 2000GB-0021524.
 PR 06-SEP-2000; 2000GB-0021894.
 PR 25-SEP-2000; 2000GB-0023444.

XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Foord SM, Ignar DM;
 XX
 PI WPI: 2002-511268/55.
 XX P-PSDB; ABB83819.
 DR
 XX
 XX An isolated P2Y-like receptor polypeptide (HIPHM 0000037) which can be
 PT used for the identification of agonists and antagonists which may be
 PT used to treat an immune or inflammatory disease -
 XX
 XX Claim 5; Page 28-29; 35pp; English.
 PS
 XX The invention relates to an isolated P2Y-like receptor polypeptide
 CC (ABB83818-ABB83819) which is also referred to in the specification as
 CC HIPHM 0000037. An effective amount of a substance (agonist or
 CC antagonist) which modulates P2Y receptor activity is useful to treat a
 CC subject having a disorder that is responsive to P2Y-like receptor
 CC modulation. The disorder is a disease of immunity or inflammation. The
 CC substance may also be used to manufacture a medicine for the treatment or
 CC prophylaxis of a disorder that is responsive to stimulation or modulation
 CC of P2Y-like receptor activity. Disorders which may be treated include
 CC colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,
 CC gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative
 CC colitis, rheumatoid arthritis, viral diseases, bacterial infections,
 CC autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic
 CC rhinitis, inflammatory pain and general inflammation such as tendonitis,
 CC polymyositis or prostatitis. The invention provides alternative
 CC substances for the treatment of immunological and inflammatory diseases.
 CC The present sequence is that the P2Y-like receptor variant encoding gene
 CC of the invention.
 XX
 XX SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;
 Alignment Scores:
 Pred. No.: 4,97e-145 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0
 US-10-023-775B-2 (1-337) x ABB85630 (1-1014)
 DY 1 MetanngluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 DB 1 ATGAATGAGCCACTGACTATTACCAATGCTTCTGATTCCCGATTATGCAGCTGCT 60
 QY 21 PheGlyAsnGlyThrAspGluAsnLeuProLeuLysMetHisTyrLeuProValIleTyr 40
 DB 61 TTTGGAAATGTCACATGATGAAGAACATCCACCTCAAGATGACTACCTCCCTTATTTAT 120
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 121 GGCATTATCTTCCTCGTGGATTCAGGCAATGAGATGATATTCACACTTACATTTC 180
 QY 61 LysMetArgProTyrPlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 181 AAAATGAGACCTTGGAAAGACGACGACCATATTATGCTGACCTGCGACAGATCTG 240
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrPhe 100
 DB 241 CTGATCTGACCAAGCTCCCTCTCTGATTCACATCAATGCGAGTGGCAAAACTGATC 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 301 TTTGGAGATTTCATGATGAAGTTATTCGCTTACACTTCACATTCACCTGTATAGCAGC 360
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 DB 361 ATCCTCTTCCCTACCTGTTTCAGCATCTTCGCGTACTGTGATCATTCACCAATAGAGC 420

QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaIaCysAlaValAlaValIleIle 160
 DB 421 TCGTTTTCATTCACAAACCTGATGATGAGTGTAGCTGTGATGATGATGATGATGAT 480
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCACGTGTGATGATTCATTCGATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrPyrAsnLeu 200
 DB 541 TCAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 601 ATTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 661 ATTATCCACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 721 AGGCTTACACTTCTGCTACTCTGCTGATTTTACGATGATGATGATGATGATGATGATGAT 780
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 781 AGGGTCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 841 CATGAAGCTTACATCTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 961 GTTACGCGGACACTTGCAGCAACCAAGAAATATTAGTTACTCAACACACCT 1011
 RESULT 5
 AAD34278
 ID AAD34278 standard; cDNA; 1014 BP.
 XX
 AC AAD34278;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE Human AXOR89 (G-protein coupled receptor) cDNA.
 XX
 KW Human; AXOR89 polypeptide; G-protein coupled receptor; vaccine; receptor;
 KW Infection; cancer; pain; asthma; Parkinson's disease; diabetes; obesity;
 KW anorexia; bulimia; acute heart failure; hypotension; hypertension; ulcer;
 KW stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia;
 KW myocardial infarction; allergy; benign prostatic hyper trophy; migraine;
 KW vomiting; psychotic; neurological disorder; anxiety; manic depression;
 KW delirium; Huntington's disease; Gilles de la Tourette's syndrome;
 KW dementia; dyskinesia; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1014
 FT /tag= a
 FT /product= "Human AXOR89 protein"
 XX
 PD GB2365012-A.
 XX
 PD 13-FEB-2002.
 XX
 PF 10-MAY-2001; 2001GB-0011437.
 XX
 PF 11-MAY-2000; 2000US-0569137.
 XX

XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM P.L.C.
 XX
 XX Elshourbagy N, Shabon U;
 DR WPI: 2002-332558/37.
 DR P-PSDB: AAE21803.
 XX
 XX Novel AXOR89 polypeptide and polynucleotide encoding it, useful for
 PT identifying agonists and antagonists in the treatment of diseases
 PT associated with an AXOR89 imbalance, such as cancers, diabetes or
 PT asthma -
 XX
 XX Claim 2: Page 30; 37pp; English.

XX The invention relates to an isolated AXOR89 polypeptide (G-protein
 CC coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide
 CC and polynucleotide encoding the polypeptide, is useful for identifying
 CC agonists and antagonists (or inhibitors) that are potentially useful in
 CC treating conditions associated with an AXOR89 imbalance, such as
 CC bacterial, fungal or protozoan infections, cancers, pain, asthma,
 CC Parkinson's disease, diabetes, obesity, anorexia, bulimia, acute heart
 CC failure, hypotension, hypertension, urinary retention, osteoporosis,
 CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign
 CC prostatic hypertrophy, migraine, vomiting, psychotic and neurological
 CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia,
 CC dyskinesias, such as Huntington's disease or Gilles de la Tourette's
 CC syndrome. The polynucleotide sequence may also be used for chromosome
 CC localisation or tissue expression studies. The AXOR89 is used as a
 CC vaccine or to produce fusion proteins. The present sequence is human
 CC AXOR89 cDNA.
 CC
 XX Sequence 1014 BP: 259 A; 263 C; 188 G; 304 T; 0 other;

Alignment Scores:

Pred. No.: 4.97e-145 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-10-023-775b-2 (1-337) x AAD34278 (1-1014)

QY 1 MetasngluProleuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 DB 1 ATGATATGAGCCATAGACTATTAGCAATCTCTGATTTCCCGATATGACAGCTCT 60
 QY 21 PheGlyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
 DB 61 TTGTGGAATGTCACATGATGAAACATCCCACTCAAGATGACACTCTCTGATATTAT 120
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 121 GGCAATATCTCTCGTGGGATTTCCAGGCAATCAGATGATGATCCACTTAACTTTTC 180
 QY 61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnAlaCysThrAspLeu 80
 DB 181 AAATGAGACCTTGGAAGAGACAGACCATCATTTATGCGAACCCTGGCTGCACAGATCTG 240
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyIleAsnTyrIle 100
 DB 241 CTGATATCTGACACACCTCCCTCTCTGATTCATCATATGACAGGGGAAACTGATC 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 301 TTGTGAGATTTCAAGTGTATGATTCGCTTCAGCTTCCATTTCAACCTGTATAGCAGC 360
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 DB 361 ATCCTCTTCTCACCCTGTTTCAGCATCTCCGCTACTGATGATGATCATTCACCAATGAGC 420

QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValIleTyrIle 160
 DB 421 TGCTTTTCATTCACAAACATGCATGTGCACTTGTAGCTGTGCTGTGATCAT 480
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCACGTGAGCTGTGATTCGATGACCTCTTGTATCATCATACACAGACAGACAGAGA 540
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspIleuAsnThrIleTyrIleTyrAsnLeu 200
 DB 541 TCAGCTCTCTCGACACTCACCAGTTCGATGATCACTATCTATTAAGTGTACACCTTA 600
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThr 220
 DB 601 ATTTGACTGCACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 661 ATTTATCCACACTCTGACCCATGACAGCTGCAAACTGACAGCTCTTAAGCAGAAAGCAG 720
 QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 721 AGGCTAACCACTTCTGCTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 781 AGGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaIleuAsnThrPheGlyAsnLeuLeu 300
 DB 841 CATGAGCTTACATCTGCTTCTGATGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
 QY 301 LeuTyrValIleValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 961 GTAAGCGGACCTTGAGCAAGCAAAATATTGTTACTCAACCAACCCCT 1011
 RESULT 6
 ID ABRK11381 standard; DNA; 1014 BP.
 XX ABRK11381;
 AC XX
 DF 05-JUN-2002 (first entry)
 DE Human DNA encoding P2Y1-like G protein-coupled receptor.
 XX Human; ds; gene; P2Y1-like G protein-coupled receptor; GPCR;
 KW Infection; pain; cancer; anorexia; bulimia; asthma; hypotension;
 KW central nervous system disease; acute heart failure; hypertension;
 KW urinary retention; osteoporosis; diabetes; angina pectoris;
 KW myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis;
 KW benign prostatic hypertrophy; psychosis; neurological disorder;
 KW dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder;
 KW Parkinson's disease; anxiety; schizophrenia; manic depression; delirium;
 KW dementia; severe mental retardation; Huntington's disease;
 KW Tourette's syndrome.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1014
 FT /*tag= a
 FT /product= "P2Y1-like GPCR"
 FN MO200214511-A2.
 XX 21-FEB-2002.
 PD 10-AUG-2001; 2001WO-EP09243.
 PF

XX 14-AUG-2000; 2000US-224989P.
PR
XX
XX (FARB) BAYER AG.
PA
XX
XX Ramakrishnan S;
PI
XX
XX WPI; 2002-257607/30.
DR P-PSDB; AAU77600.
DR

Novel human P2Y₁-like G protein-coupled receptor polypeptide which can be regulated for treating infection, pain, cancer, diabetes, anorexia, asthma, hypertension, neurological disorder and dyskinnesia

CC The invention relates to a purified human P2Y1-like G protein-coupled
CC receptor (GPCR) polypeptide and the nucleic acids encoding it
CC (including 5' and 3' sequences, promoters, fragments, variants, or a
CC sequence encoding a protein at least 50% identical to the GPCR).
CC Also included are an expression vector comprising the nucleic acid,
CC a host cell containing the vector and the identification of modulators of
CC the GPCR especially those that reduce the activity of the GPCR.
CC The nucleic acid is useful for detecting a polynucleotide encoding
CC the GPCR in a biological sample. The GPCR and nucleic acid are useful for
CC screening for agents which decrease the activity of the GPCR and
CC for modulators of the GPCR. The modulator or agent useful for modulating
CC the activity of P2Y1-like G protein-coupled receptor in a disease such as
CC bacterial, fungal, protozoan, and viral infection, pain, cancer,
CC anorexia, bulimia, asthma, central nervous system (CNS) disease, acute
CC heart failure, hypotension, hypertension, urinary retention,
CC osteoporosis, diabetes, angina pectoris, myocardial infarction, ulcer,
CC inflammation, allergy, multiple sclerosis, benign prostatic hypertrophy,
CC psychotic and neurological disorders, dyskinesias, HIV virus infection
CC (human immunodeficiency virus), CNS disorders such as Parkinson's
CC disease, anxiety, schizophrenia, manic depression, delirium, dementia,
CC severe mental retardation, Huntington's disease and Tourette's syndrome.
CC The present sequence encodes the P2Y1-like GPCR of the invention.

SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Alignment Scores:	
Pred. No.:	4.97e-145
Score:	1771.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	24
Length:	101
Matches:	337
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-023-775B-2 (1-337) x ABK11381 (1-1014)

QY MetAsnGIpProleuaspIyrleuulalaasnalaaserasphepcoaspyralaala 20
Db 1 ATGAAATGACGACCTAGACTATTAGCAAAATGCTTGTGATTTCCCGATTATGACAGCTGT 60
QY PheGIyAsnCysThrAspGIuAsnIleProleuLysMetHisTyrLeuProValIleTyr 40
Db 61 TTGGAATAATGGACATGATGAAAAACATCCOACATCAAGATGACATCCTCCGTATTAT 120
QY 41 GlyIleIlePheleuValGIyPheProGIyAsnAlaValIleSerHisTyrIlePhe 60
Db 121 GGCATTATCTTCCTCGTGGAATTTCCAGGCAATGACGATGAGTAATCCACTTACATTTC 180
QY 61 LysMetArgProTyrIlySerSerHisIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
Db 181 AAAATAGACCTTGGAGAGCAGCACCATCATTAATGCTGAACCTGGCCCTGCACGATCTG 240
QY 81 LeuTyrLeuThrSerLeuProPheleuIleHisTyrTyrAlaSerGIyGIuAsnTrpIle 100
Db 241 CTGTATCTGCACGACCTCCCTTCTGATTCATCTGATGCAAGGGGCAAAACTGGATC 300
QY PheGIyAspMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSer 120

Db	301	TTTTGAGATTTCATGTAAGTTTATTC	CCGCTTCAGCTTCATTC	CAACCGTATACGAC	360	
QY	121	IIleuPheLeuThrCysPheSerIlePhe	ArgTyrCysValIleIleHisP	PrometSer	140	
Db	361	ATCCCTTCCTCCACCTGGTTTCAG	CAACTCCCGCTACTGTGTATTC	ACCAATGAGC	420	
QY	141	CysPheSerIleHisLysThrArgCys	AlaIleValAlaCysAlaValAla	ITPPIIle	166	
Db	421	TGCTTTTCATTCACAAACTCGATG	AGTGTGAGCTGTGCTGTGGTGAT	TCATT	480	
QY	161	SerLeuValAlaValIleP	romethrPheLeuIleThrSer	ThrAsnArgThrAsnArg	180	
Db	481	TCACGTGTAAGCTGCTATTC	CGATGACCTTCGTATACATCA	CAACCAAGACACAGAC	540	
QY	181	SerAlaCysLeuAspLeuThrSer	SerAspGluLeuAsnThrIle	LysTyrPyrAsnLeu	200	
Db	541	TCAGCCTGCTCGACCTCACCA	AGTTGGATGGAATCAATCAT	TAATTAAGTGTACAACTG	600	
QY	201	IleLeuThrAlaIleThrPhe	CysLeuProLeuValIleVal	ThrLeuCysTyrThrThr	220	
Db	601	ATTTCAGCTGCACACTTTC	TGCTCCCTGGGATATGTGAC	ACTTGTGCTATACACG	666	
QY	221	IleIleHisThrLeuThrHis	GlyLeuGlnThrAspSerCys	LeuLysGlnLysAlaArg	240	
Db	661	ATTATCCACACTCTGACCC	ATGAGCTGCAAACTGACAGCT	GCCTTAAGCAAGAAAC	720	
QY	241	ArgLeuThrIleLeuLeuLeu	LeuAlaPheTyrValCysP	heLeuProPheHisIleLeu	260	
Db	721	AGGCTAACCATCTCTGACT	CTCTGATTTTACGATTTT	TATTTTACCTTCATCTTG	780	
QY	261	ArgValIleIleArgIleGlu	SerArgLeuLeuSerIleSer	CysSerIleGluAsnGlnIle	280	
Db	781	AGGGCATTCGGATCGAAT	CTCGCTTCATCATCAGTTG	CCATTGAGAAATCAGATC	840	
QY	281	HisGluAlaTyrIleVal	SerArgProLeuAlaIle	AsnThrPheGlyAsnLeuLeu	300	
Db	841	CATGAAGCTTACATGTTT	CTTAGACCATTAAGCTGCT	CTAGAACCTTTGGTAAC	900	
QY	301	LeuTyrValIleValSer	AspAsnPheGlnGlnAla	ValAlaCysSerThrVal	ArgCysLys	320
Db	901	CTATATGTGTGTGTCAG	GACAACTTTCAGCAGCGT	GTGTGCTCAACAGTGA	ATGCAAA	960
QY	321	ValSerGlyAsnLeuGlu	GlnAlaLysLysIleSer	TyrSerAsnAsnPro	337	
Db	961	GTAAGCGGGAACCTTG	AGCACAAGAAATAATTA	GTACTCAAAACAACT	1011	
RESULT 7						
AAK98323	ID	AAK98323	standard; cDNA; 1014 BP.			
XX	AAK98323;					
XX	30-APR-2002	(first entry)				
DE	Human	purinergic/-related G-protein coupled receptor (GPCR) cDNA sequence.				
XX	Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;					
KW	signal transduction; human protease; GPCR disorder; gene therapy;					
KW	transgenic animal; gene; ss.					
XX	Homo sapiens.					
OS						
XX	Key	Location/Qualifiers				
XX	CDS	1..1014				
FT	/tag-	a				
FT	/product-	"G-protein coupled receptor"				
XX	WO200187980-A2.					
XX	22-NOV-2001.					
PD	17-MAY-2001; 2001WO-US15957.					
XX						


```

XX DE Human P2Y1-11 encoding cDNA.
XX KM Human: P2Y1-11; chromosome 13; G protein-coupled; receptor;
XX KM gene therapy; thyroid; gene; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 18..1031
XX FT /*tag= a
XX FT /product= "P2Y1-like purine receptor"
XX PD DEL0046970-A1.
XX PD 11-APR-2002.
XX PF 22-SEP-2000; 2000DE-1046970.
XX PR 22-SEP-2000; 2000DE-1046970.
XX PA (BRUE/) BRUESS M.
XX PA (BOEN/) BOENISCH H.
XX PA Bruess M, Boenisch H;
XX DR MPI; 2002-353329/39.
XX DR P-PSDB; ABB79438.
XX PT New human P2Y111 gene, useful for treatment and diagnosis of associated
XX PT diseases, and related proteins, antibodies and modulators, encodes G
XX PT protein-coupled receptor
XX PS Claim 5; Page 3; 5pp; German.
XX CC The invention relates to the human P2Y111 gene (I), including its 5' and
XX CC 3' untranslated regions, located on chromosome 13 and encoding a G
XX CC protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies
XX CC etc., are used for diagnosis and (gene) therapy of diseases that are
XX CC (in)directly associated with (I) or its expression products. No diseases
XX CC are specified but as (I) is expressed only in thyroid tissue, (I) is
XX CC presumed to be involved in regulation of thyroid function. The present
XX CC sequence is that of the P2Y111 encoding cDNA.
XX SQ Sequence 1288 BP; 347 A; 318 C; 241 G; 382 T; 0 other;

Alignment Scores:
Pred. No.: 6 68e-145 Length: 1288
Score: 1771.00 Matches: 337
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Caps: 0

US-10-023-775B-2 (1-337) x ABL56197 (1-1288)
QY 1 MetaNgiubProleuaspTYrLeuAlaAsnAlaSerAspPheProAspTYrAlaAlaA 20
Db 18 ATGATGAGCCACTAGACCTATTAGCAATGCTCTGATTCCCGCATTTATGACGCGCT 77
QY 21 PheGlyAsnCystrAspGluAsnIleProleuLysMethIstYrLeuProValIleTyr 40
Db 78 TTGGAAATTCGACTGATGAAACATCCACTCAAGATGACACTCCCTGTTATTTAT 137
QY 41 GYlIlellePheLeuValIglYpHeProGlyAsnAlaValIleSerThrTyrIlePhe 60
Db 138 GGCATTATCTTCTCGTGGGATTTCCAGCAATGCACTAGATCATCCACTTACATTTTC 197
QY 61 LysMetArgProTrpIlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
Db 198 AATATGAGACCTTGGAAAGACAGACATCATTTATGCTGAACCGGCGCTGCACAGATCTG 257
QY 81 LeuTYrLeuThrSerLeuProPheLeuIleHisTYrTYrAlaSerGlyGluAsnTrpIle 100

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Db 258 CTGATATCTGACACCCCTCCCTCTGATTCACACTACTATGCATGGCGAAACTGATC 317
QY 101 PheGlyAspPheMetCysIlySrpheIleArgPheSerPheHisPheAsnLeuTYrSerSer 120
Db 318 TTTCGAGATTTTCATGCTTAAGTATTATCCGCTTCACCTTCCATTTCAACCTGTATAGCAGC 377
QY 121 IleuPheLeuThrCysPheSerIlePheArgTYrCysValIleIleHisPrometSer 140
Db 378 ATCCTCTCCACACTCTTTCACAGATCTCCGCTAGCTGATGATGATTCACCAATGAGC 437
QY 141 CysPheSerIleHisIlySrpThrArgCysAlaValAlaIlyCysAlaValIleTyrIle 160
Db 438 TGCCTTTCATTCACAAACTCGATGCAAGTTGTACTCTGCTGGTGATGATCAT 497
QY 161 SerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
Db 498 TCAGTGTAGCTGTCATTCGATGACCTCTTCTGATCACAATCAACCAAGACAGACAGAGA 557
QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleIlySrpTYrAsnLeu 200
Db 558 TCAGCTGTCTCGACCTCAGACAGTGGGATGAACTCAATCATATTAAGTGTACCAACTG 617
QY 201 IleuThrAlaThrThrPheCysLeuProleuValIleValIleLeuCysTYrThrThr 220
Db 618 ATTTGACTGCACACTACTCTTCTGCTCCCTGGTGATGAGACACTTCTATACACAGC 677
QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuIlySrpIlyAlaArg 240
Db 678 ATTATCCACACTCTGACCCAGTACGACCTCAAACTGACAGCTGCTTAAAGCAGAAAGCAGCA 737
QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTYrValCysPheLeuProPheHisIleLeu 260
Db 738 AGGCTACCATTTCTGCTACTCCCTTGCATTTAGCTATGTTTATACCTTCACATATCTTG 797
QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
Db 798 AGGCTCATTTGGGATCGAATCTCGCTCTTCAATCAGTTGTTCCATTGGAATCAAGATC 857
QY 281 HisGluLeuTYrIleValSerArgProleuAlaIleLeuAsnThrPheGlyAsnLeuLeu 300
Db 858 CATTAACCTTACATGCTTTCTAGACCATTTAGCTCTGTGAAACCTTTGGTAACCTGTTA 917
QY 301 LeuTYrValValIleSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysIlyS 320
Db 918 CTATATGTGGTGGTGCAGCAGCAACTTTCAGAGAGCTGTGCTCAACAGATGATGCAAA 977
QY 321 ValSerGlyAsnLeuGluGlnAlaIlySrpIleSerTYrSerAsnAsnPro 337
Db 978 GTAAGCGGGAACCTTGGAGCAAGCAAAAGAAATTAATTATCAACCAACCTT 1028

RESULT 10
ABL56198 standard; DNA; 5435 BP.
ID ABL56198
AC ABL56198;
XX 05-JUL-2002 (first entry)
XX DE Human P2Y1-11 encoding genomic sequence.
XX KW Human: P2Y1-11; chromosome 13; G protein-coupled; receptor;
XX KW gene therapy; thyroid; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 3188..4201
XX FT /*tag= a
XX FT /product= "P2Y1-like purine receptor"
XX PN DEL0046970-A1.

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PD 11-APR-2002.
XX
PF 22-SEP-2000; 2000DE-1046970.
XX
PR 22-SEP-2000; 2000DE-1046970.
XX
PA (BRUE/) BRUESS M.
PA (BOEN/) BOENISCH H.
XX
PI Bruess M, Boenisch H;
XX
DR WPI; 2002-353329/39.
DR P-PSDB; ABB79438.
XX
PF New human Pzyl1 gene, useful for treatment and diagnosis of associated
PT diseases, and related proteins, antibodies and modulators, encodes G
PT protein-coupled receptor -
XX
PS Claim 1; Page 4-5; 5pp; German.

PR 08-AUG-2000; 2000US-0634656.
 XX (APPL-) APPLERA CORP.
 PI Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;
 XX WPI: 2002-075312/10.
 DR P-PDB; AAO14027.
 XX Novel isolated G-protein coupled receptor peptide useful for treating
 PT disorder characterised by absence of, in appropriate or unwanted
 PT expression of the receptor protein, and as immunogens to raise
 PT antibodies -
 XX Claim 23; Fig 3; 64p; English.

XX The present specifically claimed human genomic DNA sequence (located on
 CC chromosome 13) encodes a putative-related G-protein coupled receptor
 CC (GPCR) of the invention. GPCRs constitute a major class of proteins
 CC responsible for signal transduction within a cell. Upon binding of a
 CC ligand to the extracellular portion of a GPCR, a signal is transduced,
 CC resulting in a biological or physiological change within the cell. The
 CC GPCR proteins can be divided into five families, family I contains the
 CC putative GPCRs (e.g. the P2Y receptors). P2Y receptors are
 CC characterised by their selective responsiveness towards ATP and its
 CC analogues, some also respond to UTP. The invention comprises a human
 CC G-protein coupled receptor protein and encoding nucleic acids. The GPCR
 CC protein and nucleic acids of the invention are useful in the treatment of
 CC a disease or condition mediated by a human protease. The GPCR protein of
 CC the invention is useful for the development/identification of
 CC therapeutic proteins; assays designed to quantitatively determine levels
 CC of the protein in biological fluids; identifying compounds which modulate
 CC the activity of the GPCR, or the interaction of the GPCR and a molecule
 CC with which it normally interacts; and treating a disorder characterised
 CC by an absence of, or inappropriate expression of the GPCR protein. The
 CC GPCR nucleic acids of the invention are useful in: diagnostic assays to
 CC identify changes in the GPCR nucleic acid that lead to pathology;
 CC controlling GPCR expression; and in gene therapy to treat patients with
 CC aberrant GPCR gene expression. The GPCR nucleic acids can also be used in
 CC the production of transgenic animals.

XX Sequence 9905 BP; 2656 A; 2218 C; 2061 G; 2970 T; 0 other;

Alignment Scores:

Pred. No.: 8.37e-144 Length: 9905
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 24 Gaps: 0

US-10-023-775b-2 (1-337) x AAK98324 (1-9905)

QY 1 MetAsnGluProLeuAspTyrLeuAlaAsnAlaSerSphProAspTyrAlaAla 20
 DB 8309 ATGAAATGAGCAGCTAGCTATTTAGCAAAAGCTTCTATTTCCCGATTTAGCGCTGCT 8368
 QY 21 PheGlyAsnGlyThrAspGluAsnIleProLeuIleuMetHisTyrLeuProValIleTyr 40
 DB 8369 TTGGAAATGAGCTAGCTATTTAGCAAAAGCTTCTATTTCCCGATTTAGCGCTGCT 8428
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 8429 GGCATTAATCTCTCCGCGGATTTCCAGCAATGACAGTATGATACCTTACATTTTC 8488
 QY 61 LysMetArgProIlePheSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 8489 AAAATGAGACCTTGGAGAGACACCATCATTAATGCTGAACCTGGCTCCACAGATCTG 8548
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrIle 100
 DB 8549 CTGTATCTGACCGACCTCCCTTCCTGATTCACCTACTACTAGTCCAGAGGCGAAACTGATC 8608

QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 8609 TTGGAGATTTTCATGTAAGTATATCCGGCTTCAGCTTCCATTTCAACAGCTGATATGACG 8668
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSer 140
 DB 8669 ATCTCTCCCTCCACCTGTTTCAGCATCTCCGCTACGCTGATGATCATTCACCAATGAGC 8728
 QY 141 CysPheSerIleHisTyrThrArgCysAlaValAlaValIleValIleTyrIleIle 160
 DB 8729 TGCCTTCCATTCACAAACTCCATGTCAGCTGTACCTGCTGCTGCTGCTGCTGCTGCTGCT 8788
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleHisSerThrAsnArgThrAsnArg 180
 DB 8789 TCACCTGATGCTGATCCGATGACCTCTTGTATCATCATCAACCAACAGACCAACAGA 8848
 QY 181 SerIleAsnLeuAspLeuThrSerSerAspGluLeuAsnThrIleTyrIleTyrAsnLeu 200
 DB 8849 TCACCTGCTGCTGACCTCCACAGCTCCGATGCAATCATTAAGTGTACCAACCTG 8908
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValIleThrLeuCysTyrThrThr 220
 DB 8909 ATTTGACTGCACTACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8968
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuGlyGlnAlaArg 240
 DB 8969 ATTTACCACTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 9028
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 9029 AGGTTAACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9088
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 9089 AGGTCATTTGGAGATCGAATCTCCGCTCTTCAATCATGATGTTCCATGGAATCAATC 9148
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 9149 CATGAACCTTACATCATCTTCTAGACCATTTAGCTCTCTGAAACCTTGGTAACTGTTA 9208
 QY 301 LeuTyrValAlaValSerAspAsnPheGlnGlnAlaValIleSerThrValArgCysLys 320
 DB 9209 CTATATGTGTGTGTCACGACCACTTTCACAGGCTGTGCTCAACAGTGAAGTGCAGAA 9268
 QY 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 9269 GTAAAGCGGAACCTTGAGCAAGCAAGAAATTAATTAATTAATTAATTAATTAATTAATTA 9319
 RESULT 12
 ID AAS08362 standard; cDNA; 1729 BP.
 XX AAS08362:
 AC AAS08362:
 XX 26-SEP-2001 (first entry)
 DE Human cDNA encoding G-protein coupled receptor, GPCR 39404.
 XX Human: G-protein coupled receptor; GPCR: 39404; immunogen: antibody;
 KW Good pasture's syndrome; viral hepatitis; Alzheimer's disease; lymphoma;
 KW Heymann nephritis; Paget's disease; Crohn's disease; endometriosis;
 KW systemic lupus erythematosus; actinic keratosis; myocarditis;
 KW Kawasaki syndrome; DiGeorge syndrome; peripheral B-cell neoplasm;
 KW inflammations; teratoma; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 294..1307
 FT CDS
 FT /tag= a
 FT /product= "protein 39404"
 XX PN W0200149847-A2.

XX 12-JUL-2001.
 PD 22-DEC-2000; 2000WO-US35309.
 XX 30-DEC-1999; 99US-0475790.
 PR (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Glucksmann MA, white D;
 PI WPI: 2001-432880/46.
 DR P-PSDB: AA004584.
 XX
 PT Novel isolated 26904, 38911 and 39404 polypeptides which are seven
 PT transmembrane proteins belonging to superfamily of G-protein-coupled
 PT receptors, useful for treating disorders of spleen, lung, liver, brain
 PT and kidney -
 PS
 XX Claim 2; Fig 1; 16pp; English.

CC The sequence encodes a novel human seven transmembrane domain
 CC protein belonging to the G-protein coupled receptor (GPCR) superfamily,
 CC protein 39404. The receptor is useful in drug screening assays, to
 CC identify compounds that modulate receptor activity and/or interact with
 CC the receptor, and for producing antibodies specific for the receptor, its
 CC regions or fragments. The receptor is useful for treating/diagnosing a
 CC 26904, 38911 and 39404 protein-associated disorder characterized by
 CC aberrant expression or activity of the protein, for monitoring
 CC therapeutic effect during clinical trials and other treatment, as bait
 CC proteins in a two-hybrid or three-hybrid assay, and in pharmacologic
 CC analysis. The proteins and nucleic acids encoding them are useful for
 CC diagnosis and treatment of disorders selected from disorders of the
 CC spleen, lung such as Good pasture's syndrome, liver such as viral
 CC hepatitis, brain such as Alzheimer's disease, hematopoietic stem cells
 CC such as lymphoma, kidney such as Heymann nephritis, bone such as Paget's
 CC disease, colon such as Crohn's disease, uterus and endometrium such as
 CC endometriosis, T-cell disorders such as systemic lupus erythematosus,
 CC diseases of the skin such as actinic keratosis, disorders of the heart
 CC such as myocarditis, disorders involving blood vessels such as Kawasaki
 CC syndrome, disorders involving the thymus such as DiGeorge syndrome,
 CC disorders involving B-cells such as peripheral B-cell neoplasms,
 CC disorders of the breast such as inflammations, and disorders involving
 CC the testis and epididymis such as teratoma. Numerous examples of
 CC each type of disorder are given in the specification.

XX Sequence 1729 BP; 461 A; 403 C; 302 G; 563 T; 0 other;

Alignment Scores:

Pred. No.: 3,91e-144 Length: 1729
 Score: 1764.00 Matches: 336
 Percent Similarity: 99.70% Conservative: 0
 Best Local Similarity: 99.70% Mismatches: 1
 Query Match: 99.60% Indels: 0
 DB: 22 Gaps: 0

US-10-023-775B-2 (1-337) x AAS08362 (1-1729)

QY 1 MetaAngluProleuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 DB 294 ATGAATGAGCCACTGACTATTAGCAAAATGCTTGATTTCCCGCATATGAGCTGCT 353
 QY 21 PheGlyAsnGlyThrAspGluAsnIlePheLeuLysMetHisTyrLeuProValIleTyr 40
 DB 354 TTTGAAATTCACATGATGAAAAACATCCACATCAAGATCCACTACCTCCCTGTTATTAT 413
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleIleSerThrTyrIlePhe 60
 DB 414 GGCATTATCTCTCTGCTGGGATTTCCAGCAATGCGATGATATCCACTTACATTTC 473
 QY 61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 474 AAAATGAGACTTGGAAAGAGACACATCATTTATGCTGAACTGCGCTGCACAGATCTG 533

QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTrpIle 100
 DB 534 CTGTATCTACACAGCTCCCTCTGATTCACCTACTATGACCGAGTGGCAAACTGATC 593
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 594 TTTGAGATTTATGATGTAAGTTATCCGCTCAGCTTCACATTCACCTGATATACAG 653
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 DB 654 ATCCCTTCCTCCACCGTTTTCAGCATCTCCGCTACTGCTGATTCATTCACCAAGAGAC 713
 QY 141 CysPheSerIleHisTyrThrArgCysAlaValAlaCysAlaValAlaValTrpIleIle 160
 DB 714 TGTCTTTCATTCACAAACCTCATGTGACGTTGACCTGTGCTGTGATGATTCATT 773
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 774 TCACGTGTAGCTGTCTATTCGATGACCTTCCTTGATCATCATCAACCAAGAGACAG 833
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTyrAsnLeu 200
 DB 834 TCAGCCTGTCTGACCTTCACAGTTGGAATCAATATATTAAGTGATACCAACTG 893
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 894 ATTTTACGACACTCTTCTGCTCCCTTGATATGATGACACTTGTGATACACG 953
 QY 221 IleIleHisThrLeuThrThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 954 ATATCCACACACTGTGACCATGACATGCAAGATGACAGCTGCTTAAAGCAAGACAGCA 1013
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 1014 AGGCTTACCATCTCTGCTACTCTGCTGATTTAGTATGTTTATACCTTCCATATCTTG 1073
 QY 261 ArgValIleArgIleGlnSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 1074 AGGCTATTCGATGCAATCTGCTGCTTTCATATGATGATGATGATGATGATGATGAT 1133
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 1134 CATGAAGCTTACATGCTTCTTGACCATTAAGCTGTGAACACCTTGTGATACCTGTTA 1193
 QY 301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 1194 CTATATGTGTGTGTGTCAGCACAACCTTTCAGCAGGCTGTCTGCTCAACAGTGAATCMAA 1253
 QY 321 ValSerGlyAsnLeuGlnGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 1254 GTAAAGGGAGAACCTTGAGCAAGCAAAAGAAATAGTTACTCAAAACACCT 1304

RESULT 13
 ABV24026
 ID ABV24026 standard; cDNA; 1729 BP.
 XX
 AC ABV24026;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 24017.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.

XX 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 PS Claim 1; Page 4453-4454; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;
 Alignment Scores:
 Pred. No.: 3,91e-144 Length: 1729
 Score: 1764.00 Matches: 336
 Percent Similarity: 99.70% Conservative: 0
 Best Local Similarity: 99.70% Mismatches: 1
 Query Match: 99.60% Indels: 0
 DB: 23 Gaps: 0
 US-10-023-775b-2 (1-337) x ABV24026 (1-1729)
 QY 1 MetasglnuProleuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 DB 294 ATGAATGAGCCACTAGACTATTGACAAATGCTTCTGATTTCCCGGATTAAGAGCTGCT 353
 QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuIleuMetHisTyrLeuProValIleTyr 40
 DB 354 TTGGGAATTCGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTTAT 413
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 414 GGCATATCTCTCCGCGGATTTCCAGCAATGCACTAGATGATCCACTTACATTTC 473
 QY 61 LysMetArgProTrpPheSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 474 AAATATGACCTTGGAAGACAGACCATCATTAATGTAACCTGGCCCTGACAGATCTG 533
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrIle 100
 DB 534 CTGTATCTGACGACCTCCCTTCCTCATTCACACTACATGCGGCGGAAACTGGATC 593
 QY 101 PheGlyAspPheMetCysTyrPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 594 TTGGAGATTTCAATGTTAGTTATCCGCTTCAGCTTCATTTCAACCTGTAAGAGAC 653
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPrometSer 140

DB 654 ATCCTCTCCCTACCTGTTTCAGCATCTTCGCTACTGTCATCATCCCAATGAGC 713
 QY 141 CysPheSerIleHisTyrThrArgCysAlaValAlaIleCysAlaValIleTyrIle 160
 DB 714 TGCCTTTCCATTCACAAACTCCGATGCTGACCTGTGTACCTGTGGTGTGATTT 773
 QY 161 SerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 774 TCAGTGTACTGTCATTCGATGACCTTCTTGATCATCATCAACCAAGACAGACAGA 833
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleTyrTyrAsnLeu 200
 DB 834 TCAGCCCTGCTCGACCTCAGACAGTTCGAGTGAACCTCAATTAAGTGTGACAACTG 893
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValIlePheLeuCysTyrThr 220
 DB 894 ATTTGACTGCACACTTCTTCTGCTCCCTTGCTGATGATGACACTTGTCTATACACG 953
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuGlyAlaArg 240
 DB 954 ATATCCACACTGTCAGCCATGACCTGCAAACTGACAGCTGCTTAAGCAGAAAGCAGA 1013
 QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 1014 AGGCTAACCATTCCTGCTACTCTTGCACTTTAGCTAGTTTATACCTTCATATCTTG 1073
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 1074 AGGCTATTCGATGATGCAATCTCCGCTCTTCAATGCACTGTTCCATGGAATGACATC 1133
 QY 281 HisGlnAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 1134 CATGAAGCTTACATCGTTCTGCGACCATAGCTGCTGAAACACCTTGGTAACTGTGTA 1193
 QY 301 LeuTyrValIleValSerAspAsnPheGlnGlnAlaValIleSerThrValArgCysTys 320
 DB 1194 CTATATGTGTGTGTCAGCAGCACTTTCACAGGCTGTGCTCAACAGTGAAGTGCAAA 1253
 QY 321 ValSerGlyAsnLeuGluGlnAlaTyrIleSerTyrSerAsnAsnPro 337
 DB 1254 GTAAAGCGGAACCTTGAGCAAGCAAAATAATTAGTACCAAAACACCT 1304
 RESULT 14
 ABV25767 standard; cDNA; 1729 BP.
 XX ID ABV25767
 AC ABV25767;
 XX
 XX 16-SEP-2002 (first entry)
 DE
 DE Human prostate expression marker cDNA 25758.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 XX Homo sapiens.
 OS
 OS WO200160860-A2.
 PN
 PD 23-AUG-2001.
 PF
 PF 20-FEB-2001; 2001WO-US05171.
 PR
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;
 XX MPI: 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 PS Claim 1: Page 5175-5176; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other:
 Alignment Scores:
 Pred. No.: 3,91e-144 Length: 1729
 Score: 1764.00 Matches: 336
 Percent Similarity: 99.70% Conservative: 0
 Best Local Similarity: 99.70% Mismatches: 1
 Query Match: 99.60% Indels: 0
 DB: 23 Gaps: 0
 US-10-023-775b-2 (1-337) x ABV25767 (1-1729)
 QY 1 MetanngluProleuAspTyrIleuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 DB 294 ATGAATGAGCCACTGACATTTTACAAATGCTTGATTCGCCGATATACAGCTGCT 353
 QY 21 PheGlyAsnCySerAspGluAsnIleProLeuLysMetHisTyrIleuProValIleTyr 40
 DB 354 TTGGAAATGACGACGATGAAACATCCCACTCAAGATGACCTACCTCCTGTATTAT 413
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 414 GGCATTATCTCTCCTGGGATTTCCAGCAATGACAGTAGATATCCACTTACATTTTC 473
 QY 61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 474 AAAATGAGACCTTGGAGAGCAGCAGCATCATTAATGCGTGGCCGACACATCTG 533
 QY 81 LeuTyrIleuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrPile 100
 DB 534 CTGATCTGACAGCCTCCCTCTCTGATTCACHTACTATGACAGTGGCCAAAGCTGATC 593
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 594 TTTGGAGATTTCATGTAAGTTTATCCGCTTCAGCTTCATTCACCTGTATATGACAC 653
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 DB 654 ATCCCTTCCTCACCCTGTTTCAGCATCTCCCTACTGCTGATCATCAACCAATGAGAC 713
 QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValValIlePheIle 160
 DB 714 TGCCTTTCCATTCACAAAACCTGATGTCAGTGTGAGCTGTGCTGTGGATCATT 773
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 774 TCACGTGATAGCTGTGATTCGATGACCTCTTGATCAATCAACCAAGAGCAACAGCA 833

QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrPyrAsnLeu 200
 DB 834 TCAAGCTGTCTGACCTCACCACCTGGATGAATCTAAATCTATTAAAGGTACCACTG 893
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 894 ATTTGACGCAACATCTTCTGCGCCCTGGTATAGTACACTTTGCTATACACAG 953
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 954 ATTATCCACACTCTGACCCATGACACGCAAACTGACAGCTGCTTAAGCAGAAAGCAGCA 1013
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 1014 AGGCTACCATCTCTGCTACTCTGATTTAGTATGTTTATACCTTCATATCTTG 1073
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 1074 AGGCTCATTCGGATCGAATCTCGCTTTCATCATGATGTTCCATTGAGATCAGATC 1133
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 1134 CATGAAGCTTACATCTCTTCTGGACCATTAAGCTGCTGAACACCTTGATACCTGTTA 1193
 QY 301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
 DB 1194 CTATATGTGTGTGTGCGCAGCAACCTTTCAGCAGCTGTCTGCTCAACAGATGCATA 1253
 QY 321 ValSerGlyAsnLeuGlnGlnAlaLysLysIleSerTyrSerAsnPro 337
 DB 1254 GTTAAAGGGAACCTTGACGACAGCAAGAAATTAAGTTACTCAAAACACCT 1304
 RESULT 15
 ABV29909
 ID ABV29909 standard; cDNA; 1729 BP.
 XX
 AC ABV29909;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 29900.
 XX
 OS Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PD 23-AUG-2001.
 XX
 PD 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX MPI: 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 PS Claim 1: Page 6451; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 1729 BP: 461 A; 401 C; 302 G; 548 T; 17 other;

Alignment Scores:

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US-10-023-775b-2 (1-337) x ABV29909 (1-1729)

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Search completed: May 29, 2003, 23:50:23
Job time : 305 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 29, 2003, 23:11:00 ; Search time 3126 Seconds

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3137.443 Million cell updates/sec

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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1771	100.0	1014	6	AX305130 Sequence
3	1771	100.0	1014	6	AX379468 Sequence
4	1771	100.0	1014	6	AX384211 Sequence
5	1771	100.0	1014	6	AX464561 Sequence
6	1771	100.0	1014	6	AB083598 Homo sapi
7	1771	100.0	1014	9	AF411109 Homo sapi
8	1771	100.0	1081	6	AX458238 Sequence
9	1771	100.0	1092	9	AF370886 Homo sapi
10	1771	100.0	1414	9	AB065877 Homo sapi
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12	1771	100.0	67645	9	AL356486 Human DNA
13	1771	100.0	156555	9	AC026756 Homo sapi
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15	1724	97.3	1020	6	AX147840 Sequence
16	1495	84.4	202838	2	AC108794 Sequence
17	940	53.1	578	6	AX147814 Sequence
18	597	22.45	2245	6	AX384210 Sequence
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ALIGNMENTS

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 DEFINITION Sequence 27 from Patent WO0136471.
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 VERSION AX148186.1 GI:14347086
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1014)
 Chen, R., Dang, H.T. and Lowitz, K.P.
 Endogenous and non-endogenous versions of human g protein-coupled
 receptors
 Patent: WO 0136471-A 27 25-MAY-2001;
 Arena Pharmaceuticals, Inc. (US)
 FEATURES
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 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
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 DEFINITION Sequence 10 from Patent WO0187937.
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 1
 Patterson, C., Lu, D.A., Thornton, M., Lu, Y., Tribouley, C.M.,
 Graul, R., Khan, F.A., Gandhi, A.R., Walla, N.K., Nguyen, D.B., Yue, H.,
 Hafalla, A., Elliott, V.S., Lal, P., Reddy, R., Kallick, D.A., Tang, T.Y.
 and Au-Young, J.
 G-protein coupled receptors
 Patent: WO 0187937-A 10 22-NOV-2001;
 Incyte Genomics, Inc. (US)
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 AUTHORS Wei, H., Zhao, Q.C., Cravchik, A.C., di Francesco, V.C. and

TITLE Beasley, E.M.
 JOURNAL Isolated human g-protein coupled receptors, nucleic acid molecules
 Patent: WO 0187980-A 1 22-NOV-2001;
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RESULT 4
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ACCESSION AX384211
VERSION AX384211.1 GI:19577652
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Ramakrishnan S.
AUTHORS Regulation of human p2y1-like g protein-coupled receptor
TITLE Patent: WO 0214511-A 5 21-FEB-2002;
JOURNAL Bayer Aktiengesellschaft (DE)
FEATURES
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Pred. No.: 1,32e-126 Length: 1014
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Best Local Similarity: 100.00% Mismatches: 0
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QY 61 LysMetArgProTYrLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
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LOCUS AX464561 1014 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 1 from Patent EP1219638.
ACCESSION AX464561
VERSION AX464561.1 GI:21899357
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Fiddock M.D.
AUTHORS G-protein coupled receptors having homology to the p2y
TITLE purinoreceptor 1 (p2y1)
JOURNAL Patent: EP 1219638-A 1 03-JUL-2002;
Pflizer Limited (GB) ; Pflizer Inc. (US)
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 259 a 263 c 188 g 304 t
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Alignment Scores:
Pred. No.: 1,32e-126 Length: 1014
Score: 1771.00 Matches: 337
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
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DB	1 ATGAAATGAGCCACTAGACATATTAGCAAAATGCTTGTGATTTCCCGATATGACAGCTGT	60	100.00%	60	0	0	0
OY	21 PheGlyAsnCySthAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr	40	100.00%	40	0	0	0
DB	61 TTTGGAATTTGCACGATGAAACATCCACATCAAGATGACACTACCTCCCTGTATTAT	120	100.00%	120	0	0	0
OY	41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe	60	100.00%	60	0	0	0
DB	121 GGCATTATCTCTCGTGGGATTTCCAGGCAATGCAAGTATATCCACTTACATTTC	180	100.00%	180	0	0	0
OY	61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu	80	100.00%	80	0	0	0
DB	181 AAAATGAGACCTTGGAAAGACGACACATCATATGCTAAGCTGGCCGACAGATCTG	240	100.00%	240	0	0	0
OY	81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrPile	100	100.00%	100	0	0	0
DB	241 CTGTATCTGACGAGCTCCCTCTCTGATTCATGATGCGAGTGGCGAAATGATGATC	300	100.00%	300	0	0	0
OY	101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer	120	100.00%	120	0	0	0
DB	301 TTTGGAGATTTCTATGTATGATTTATCCGCTTCACCTTCATTCACCTGTATGACAC	360	100.00%	360	0	0	0
OY	121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer	140	100.00%	140	0	0	0
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DB	601 ATTTGACTGCAACTACTTCTGCTCCCTGCTGATGATGACACTTGTGATACAG	660	100.00%	660	0	0	0
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OY	241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu	260	100.00%	260	0	0	0
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OY	261 ArgValIleArgGlyLeuSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle	280	100.00%	280	0	0	0
DB	781 AGGCTCATTCGATCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840	100.00%	840	0	0	0
OY	281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeu	300	100.00%	300	0	0	0
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OY	301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys	320	100.00%	320	0	0	0
DB	901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960	100.00%	960	0	0	0
OY	321 ValSerGlyAsnLeuGlnAlaLysLysIleSerTyrSerAsnAsnPro	337	100.00%	337	0	0	0
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 1
 Takeda, S., Kadowaki, S., Haga, T., Takeasu, H. and Mitaku, S.
 Identification of G protein-coupled receptor genes from the human
 genome sequence
 Unpublished
 2 (bases 1 to 1014)
 Takeda, S., Kadowaki, S., Haga, T., Takeasu, H. and Mitaku, S.
 Direct Submission
 Submitted (10-Apr-2002) Shigeaki Takeda, Gunma University,
 Department of Biological and Chemical Engineering, Faculty of
 Engineering, 1-5-1, Kiryu, Gunma 376-8515, Japan
 (E-mail:stakeda@ce.gunma-u.ac.jp, Tel:+81-277-30-1434,
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US-10-023-775b-2 (1-337) x AB083598 (1-1014)

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DB	1 ATGAAATGAGCCACTAGACATATTAGCAAAATGCTTGTGATTTCCCGATATGACAGCTGT	60	100.00%	60	0	0	0
OY	21 PheGlyAsnCySthAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr	40	100.00%	40	0	0	0
DB	61 TTTGGAATTTGCACGATGAAACATCCACATCAAGATGACACTACCTCCCTGTATTAT	120	100.00%	120	0	0	0
OY	41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe	60	100.00%	60	0	0	0
DB	121 GGCATTATCTCTCGTGGGATTTCCAGGCAATGCAAGTATATCCACTTACATTTC	180	100.00%	180	0	0	0
OY	61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu	80	100.00%	80	0	0	0

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Qy 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
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Qy 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPrometSer 140
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DEFINITION AF411109
ACCESSION AF411109.1 GI:16566322
VERSION
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SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1014)
AUTHORS Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vantli,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
TITLE Discovery and mapping of ten novel G protein-coupled receptor genes
JOURNAL Gene 275 (1), 83-91 (2001)
MEDLINE 21458557
PUBMED 11574155

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REFERENCE 2 (bases 1 to 1014)
AUTHORS Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vantli,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2001) Department of Pharmacology, University of
Toronto, 8 Yaddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Ramanathan, C., Feder, J., Nelson, T., Cacace, A., Barber, L. and
 Rysek, R. P.
 TITLE A novel human g-protein coupled receptor, hgrbm23, expressed
 highly in kidney
 JOURNAL Patent: WO 0246414-A 1 13-JUN-2002;
 Bristol-Myers Squibb Company (US)
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BASE COUNT 280 a 277 c 198 g 326 t
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 Pred. No.: 1,41e-126 Length: 1081
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US:10-023-775b-2 (1-337) x AX458238 (1-1081)

QY 1 MetAsnGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
 Db 54 ATGATAGAGCCACATGATATTTAGCAAAATGCTTCTGATTTCCCGGATTAAGCAGCTCT 113
 QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
 Db 114 TTTGGAAATTCACATGATGAAGAAACATCCCAAGATGACATCTCCCTGTTATTTAT 173
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 Db 174 GGCATATCTTCTGCTGCTGGATTCACAGCAATGACATGATATCCATTCATTTTC 233
 QY 61 LysMetArgProTyrPlySerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 Db 234 AAAATGAGACCTTGGAAAGACGACGACCATCATTTATGTAACCTGGCTGCACAGATCTG 293
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyIleAsnTyrIle 100
 Db 294 CTGATATCGACACACCTCCCTCTCTGATTCACACTATGACATGGGGAATCGATGATC 353
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 Db 354 TTTGAGATTTTCATGCTGTAAGTTTATCCGCTTACCTTCCATTCACCTTATAGCAGC 413
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 Db 414 ATCTCTTCCTCCACCTGTTTCCAGCATCTCCGCTAGCTGTGATCATTCACCAATGAGC 473
 QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTyrIleIle 160
 Db 474 TGCCTTTCCATTCACAAACATCGATGTCACATTTAGCTGTGCTGTGGATTCAT 533
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 Db 534 TCACGTGATGTCATTCGATGACCTTCTTGATACATACCAACAGGACCAACGAGA 593
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspIleuAsnThrIleLeuIleLeuIleLeu 200
 Db 594 TCACGCTGTGTCGACCTGACCAAGTTCGGATGACCAATATATTAAGTGTACACCTG 653
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValIleThrLeuCysTyrThrThr 220
 Db 654 ATTTGACGTGCACTACTTCTGCTCCCTGCTGTGATAGACACTTGTCTATACACAG 713
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuGlnIleAlaArg 240
 Db 714 ATTTCCACACTGTGACCCAGTACGACCACTGACAGCTGCTTAAAGCAAAAGACAGA 773
 QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 Db 774 AGGCTAACCAATTCGTACTACCTTCGATTTAGCATATGTTTAACTTCATATCTTG 833
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 Db 834 AGGCTCATTCGGATCGATTCGCTCTTCATTCATTCATTCATTCATTCATTCATTCAT 893
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaIleAlaLeuAsnThrPheGlyAsnLeuLeu 300
 Db 894 CATAGACCTTCATCGTTTCTAGACCATTCAGCTGCTGAAACACCTTGGTAACTGTTA 953
 QY 301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320

Db 954 CTATATGTGGTGGTCAGCGACACTTTCAGCAGCGCTGTCTCTCAACAGTAGATGCAAA 1013

Qy 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
|||||
Db 1014 GTAGCGGGAACCTTGAGCAAGCAAGAAATATTGTTACTCAACAAACCT 1064

RESULT 9
AF370886 1092 bp mRNA linear PRI 11-JUL-2002
DEFINITION Homo sapiens G protein-coupled receptor GPR99 (GPR99) mRNA,
AF370886 complete cds.
ACCESSION AF370886
VERSION AF370886.1 GI:21728283
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1092)
Wittenberger,T., Hellebrand,S., Munck,A., Krelenkamp,H.J.,
Schaller,H.C. and Hampe,W.
GPR99, a new G protein-coupled receptor belonging to a new subgroup
of nucleotide receptors
BMC Genomics 3 (1), 17 (2002)
12098360
2 (bases 1 to 1092)
Hampe,W.
Direct Submission
Submitted (17-APR-2001) Developmental Neurobiology, Zentrum fuer
Molekulare Neurobiologie, Martinistr. Hamburg 20246, Germany

FEATURES
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1. 1092
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
1. 1092
/gene="GPR99"
19. 1032
/gene="GPR99"
/product="G protein-coupled receptor GPR99"
/codon_start=1
/protein_id="AA076912.1"
/db_xref="GI:21728284"
/translation="MNEPLDYLANASDPDYAAFGNCTDENIPLKMHLYPIVYIIF
LVGPGNAVVISYIIFKRPWKSSTIIMLNACDLYLSLPLIHVYSGENWIG
DPMKPIRFSPHNLYSILFICFSIFRCVLIHPKSCSIHTRKAVAVAVYMI
SIVAVIPMTLITSTNRTNSACIDLTSSDLNTIKWYINLTITTCCLPIYTIY
TTIHTHTHGIQDTSCUKOKARRTITILLAFYCFILPRLIRIRIESRLISCSI
ENOIHENATIVSRPLAALNTFENLLIYVSDNFQAVCSYVRKAVSGNLEQAKKISYS
NRP."

BASE COUNT 290 a 279 c 198 g 325 t

ORIGIN

Alignment Scores:
Pred. No.: 1.43e-126 Length: 1092
Score: 1771.00 Matches: 337
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-023-775b-2 (1-337) x AF370886 (1-1092)

Qy 1 MetAsnGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
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Db 19 ATGAAATAGCCACTAGACTATTATAGCAAAATGCTTCTGATTTCCCGCATATGACGCTGCT 78

Qy 21 PheGlyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
|||||
Db 79 TTGGAAATTTGCACTGATGAAGAACATCCACTCAAGATGACATGCTCCGCTATTATAT 138

Qy 41 G|Y|I|L|E|P|H|E|U|A|V|A|I|L|E|P|H|E|U|A|V|A|I|L|E|S|E|R|T|Y|R|I|L|E|P|H|E 60
|||||

Db 139 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTATATCCACTTACATTTTC 198

Qy 61 LysMetArgProTyrPlysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
|||||
Db 199 AAATGAGACCTTGGAAAGAGACACCATATATTGCGAACCTGGCCCTGCACAGATCTG 258

Qy 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrPle 100
|||||
Db 259 CTGATCTGACACACCTCCCTCTCGTATACACTATATGCGATGGGAAACCTGGATTC 318

Qy 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
|||||
Db 319 TTGGAGATTTTCATGTGTAAGTTATCCGCTTCAGCTTCACATTCATCACTGATATGAGAC 378

Qy 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
|||||
Db 379 ATCCTCTTCCACACTGTTTATAGCATCTCCGCTACGTGTGATCATTCACCCATATGAC 438

Qy 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTyrPleIle 160
|||||
Db 439 TGCCTTTCATTTCCAAACAAACATCGATGTCAGCTGTAGCCTGCTGTGTGTGATCAT 498

Qy 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
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Db 499 TCACCTGTAGCTGTGATTCGATCCGATGACCTTCTTGATCATCAACACAGACGACACAGA 558

Qy 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrTyrAsnLeu 200
|||||
Db 559 TCACCTGTCTCGACCTCCACCTCCAGTTCGGATCACTCATATTAAGTGTACACCTG 618

Qy 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
|||||
Db 619 ATTTGACTGCACTACTTCTGCTCCCTCCCTGTGTGATGAGACACTTGTGTATACACAG 678

Qy 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
|||||
Db 679 ATATCCACACTGTGACCCATGACTGCAAACTGACAGCTGCTTAAGCACAAAGACAGA 738

Qy 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrAlaCysPheLeuProPheHisIleLeu 260
|||||
Db 739 AGGCTAACCATTCCTGCTACTCTGCTGATTTTACGTATGTTTATACCTTCATATCTTG 798

Qy 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
|||||
Db 799 AGGCTCAATCGCATGCAATCGCGCTCTTCAATCAAGTTGTTCCATTGAGAAATCAATC 858

Qy 281 HisGluAlaTyrIleValSerArgProLeuAlaIleAsnThrPheGlyAsnLeuLeu 300
|||||
Db 859 CATGACCTTACATCGTTTCTAGACCATATGCTGCTCTGAAACACCTTGGTAACTCTTGA 918

Qy 301 LeuTyrValAlaValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
|||||
Db 919 CTATATGTGGTGGTCAGCGACACTTTCAGCAGCGCTGTCTCTCAACAGTAGATGCAAA 978

Qy 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
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Db 979 GTAGCGGGAACCTTGAGCAAGCAAGAAATATTGTTACTCAACAAACCT 1029

RESULT 10
AB065877 1414 bp DNA linear PRI 23-JUL-2002
LOCUS Homo sapiens gene for seven transmembrane helix receptor, complete
DEFINITION cds, isolate:CBRC7TM_440.
ACCESSION AB065877
VERSION AB065877.1 GI:21929018
KEYWORDS
SOURCE Homo sapiens (isolate:CBRC7TM_440) DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1
Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S.,
Teutsunli,S., Aburatani,H., Asai,K. and Akiyama,Y.

TITLE	genome-wide discovery and analysis of human seven transmembrane
JOURNAL	helic receptor genes
REFERENCE	unpublished
2	(bases 1 to 1414)

Alignment Scores:

Pred. No.: 1.41e-125 Length: 9905
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-023-775b-2 (1-337) x AX379470 (1-9905)

QY 1 MetAsnGluProLeuAspTyrLeuAlaAlaSerAspProAspTyrAlaAla 20
 DB 8309 ATAAATGAGCCATGAGTATTAAGCAAAATGCTTCAATTTCCCGATATGAGCGTCT 8368
 QY 21 PheGlyAsnGlyThrAspGluAsnAlaProLeuLysMetHisTyrLeuProValIleTyr 40
 DB 8369 TTGGAAATTCGACTGATGAAGAACATCCCACTCAGATGCACTACCTCCCTGTTATTTAT 8428
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 DB 8429 GGCATTATCTTCCTCGTGGGATTTCCAGCAATGCACTAGTATTCACATTTCATTTTC 8488
 QY 61 LysMetArgProThrLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 8489 AAAATGAGACCTTGAGAGACACACCATCATTAATGCTGAACCTGGCTGCACAGATCTG 8548
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyIleAsnTyrIle 100
 DB 8549 CTGTATCTGACACGCTCCCTTCCTGATTCACCTACTACTATGCGACGAAACTGATC 8608
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 DB 8609 TTGGGAGATTACAGTCTAGATTATCCGCTTCACTTCATTCACCTGATATGACG 8668
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSer 140
 DB 8669 ATCTCTCTCTCCACCTGTTTCACATCTTCCTGCTAGTGTGATCATTCACCCATAGC 8728
 QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValAlaTyrIleIle 160
 DB 8729 TGTCTTTCATTCACAAACTCATGATGCACTGTGTGCTGTGTGTGTGTGTGTGTGT 8788
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 8789 TCACGTGTGCTCTCATTCCTGATGACCTTCTGATCATCAACAACAGACCAACAGACA 8848
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrPyrAsnLeu 200
 DB 8849 TCAGCTGTCTGACCTCCACCTGATGATGATGATGATGATGATGATGATGATGATG 8908
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 DB 8909 ATTTGACGTGCACTACTTCTGCTCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 8968
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
 DB 8969 ATTATTCACACTCTGACCTGACCTGCAACTGCAAGCTGCTTAAAGCAAGCAAGCAGA 9028
 QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 DB 9029 AGGCTTACCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9088
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 DB 9089 AGGGTATTCGATCGAATCGATCGCTGCTTCAATGATGCTGCTGCTGCTGCTGCTGCTG 9148
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
 DB 9149 CAGGAGCTTACATCTGCTTCTAGACATTAAGCTGCTGCAACCTTGTGTAACCTGCTTA 9208
 QY 301 LeuTyrValValValSerAspAsnPheGlnGlnAlaValCysSerThrValAlaGlyCysLys 320
 DB 9209 CTATATGT 9268

QY 321 ValSerGlyAsnLeuGlnGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
 DB 9269 GTAAAGCGGAACTTGAGCAAGCAAAATAATTGATTACGTAACAACACCT 9319

RESULT 12
 AL356486/C
 LOCUS
 DEFINITION Human DNA sequence from clone RP11-721F14 on chromosome 13, complete sequence.

ACCESSION AL356486
 VERSION AL356486
 KEYWORDS AL356486.12 GI:15808158
 SOURCE HTG.
 ORGANISM human.
 Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 67645)

REFERENCE
 AUTHORS Skuce, C.
 TITLE Direct Submission
 JOURNAL Submitted (27-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, UK
 CH10 ISA, UK. E-mail enquiries: humgeny@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 On Sep 28, 2001 this sequence version replaced gi:15787734.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30);
 an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPep; Information on the WORMPEP
 database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 This sequence was generated from part of bacterial clone contigs of human
 chromosome 13, constructed by the Sanger Centre Chromosome 13
 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr13
 RP11-721F14 is from the library RPCI-11.3 constructed by the group
 of Pieter de Jong. For further details see
 http://www.chori.org/dacpac/home.htm
 VECTOR: pBAC3.6

IMPORTANT: This sequence is not the entire insert of clone
 RP11-721F14. It may be shorter because we sequence overlapping
 sections only once, except for a short overlap.
 The true left end of clone RP11-199B17 is at 65646 in this
 sequence. The true right end of clone RP11-651J9 is at 2000 in this
 sequence.

FEATURES
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 1. 67645
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="13"
 /clone="RP11-721F14"
 /clone_1b="RPCI-11.3"
 53919
 /note="Random repeat. Forced join. Gap size estimated to
 be approximately 110bp by restriction digest data."

misc_feature
 BASE COUNT 20542 a 13252 c 13216 g 20635 t
 ORIGIN

Alignment Scores:
 Pred. No.: 1.04e-124 Length: 67645
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-023-775b-2 (1-337) x AL356486 (1-67645)

Oy 1 MetanGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20
Db 5091 ATGAAATGAGCCACTGATATTAGCAAAATGCTTGTATTCGCCGATTATGACCTGCT 5032

Oy 21 PheGlyAsnGlySerAspGluAsnLeuProLeuGlyMetHisTyrLeuProValIleTyr 40
Db 5031 TTGGAAATTCACAGATGAGTAAACATCCCACTCAAGATGAGCACTACCTCCCTGTTAT 4972

Oy 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
Db 4971 GGCATTATCTCTCTGCTGGATTTCCAGCAATGAGATGATATCCACTTACATTTTC 4912

Oy 61 LysMetArgProTyrPheSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
Db 4911 AAAATGAGACCTTGGAAAGAGCAGACCATCATTTAGTGAACCTGCGTGCACAGATCTG 4852

Oy 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrIle 100
Db 4851 CTGATCTGACACGAGCTCCCTCTGCTGATCTACTATGCGCAGCGAAACCTGATC 4792

Oy 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSer 120
Db 4791 TTGGAGATTCATGTTGATGATTCGCTTACCTTCACCTTCACCTTCATTCACCTGAT 4732

Oy 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
Db 4731 ATCCCTCTCTCCACCTGTTTACAGATCTTCCGCTACTGCTGATCATTCACCAATGAGC 4672

Oy 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValValTyrIleIle 160
Db 4671 TGCCTTTCATTCACAAATCGATGTCAGTTGAGCTGCTGCTGCTGCTGCTGCTGCT 4612

Oy 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
Db 4611 TCACGTGAGTGTCTATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 4552

Oy 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTyrTyrAsnLeu 200
Db 4551 TCACGCTCTCTCGACCTGATCAGATGTCAGATGATGATGATGATGATGATGATGATGAT 4492

Oy 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
Db 4491 ATTTGACTGCAACTACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4432

Oy 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
Db 4431 ATTATTCACACTGTCACCATGAGTGCATGCAAACTGCACTGCTTACACAGAAACAGCA 4372

Oy 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
Db 4371 AGGCTAACCATTCCTGCTACTCTGCTGATTTACGATGATTTTTCCTTCATATCTTG 4312

Oy 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
Db 4311 AGGCTAACCATTCCTGCTACTCTGCTGATTTACGATGATTTTTCCTTCATATCTTG 4252

Oy 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
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Oy 301 LeuTyrValIleValSerAspAsnPheGlnGlnAlaValCysSerThrValArgCysLys 320
Db 4191 CTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4132

Oy 321 ValSerGlyAsnLeuGluGlnAlaLysLysIleSerTyrSerAsnAsnPro 337
Db 4131 GTAAGCGGACCTTGAGCAAGCAAAATTAATGTTACTCAAAACACCT 4081

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RESULT 13
AC026756
LOCUS
AC026756
DEFINITION
AC026756
VERSION
AC026756.15
KEYWORDS
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SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 156555)
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D.,
Feder, S.P., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R.,
Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J.,
Ramirez, D., Wilhelmy, J., Yu, S. and Davis, R.W.
Direct Submission
Submitted (23-MAR-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
TITLE
3 (bases 1 to 156555)
AUTHORS
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D.,
Feder, S.P., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R.,
Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J.,
Ramirez, D., Wilhelmy, J., Yu, S. and Davis, R.W.
Direct Submission
Submitted (23-FEB-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
COMMENT
On Feb 23, 2001 this sequence version replaced gi:12745089.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SDBTDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum.info@sequence.stanford.edu
----- Project Information
Center project name: 870
Center clone name: RP11-286P8
----- Summary
This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.
FEATURES
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/clone="RP11-286P8"
/clone_11b="RP11 human BAC library 11"
BASE COUNT
48748 a 30845 c 30755 g 46207 t
ORIGIN
Alignment Scores:
Pred. No.: 2,49e-124 Length: 156555
Score: 1771.00 Matches: 337
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

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DB: 9 Gaps: 0

US-10-023-775b-2 (1-337) x AC026756 (1-156555)

OY 1 MetAsnGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20

DB 140188 ATGAATGAGCCTAGACTATTTAGCAAAATGCTTCGATTTCCCGCATTAAGACGCT 140247

OY 21 PheGlyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40

DB 140248 TTGGAAATGACCTGATGAAACATCCCAAGTGCAGTACCTCCCTGTTATTTAT 140307

OY 41 GlyTllePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrTllePhe 60

DB 140308 GGCAATATCTTCCTCGGGGATTTCCAGCAATGCAAGTATGATTCACCTTACATTTTC 140367

OY 61 LysMetArgProThrLysSerSerThrIleIleMetLeuAsnIleuLacysThrAspLeu 80

DB 140368 AAAATGAGACCTTGGAAAGACACACCATCATTTATGCTGAACCTGGCTGCACAGATCTG 140427

OY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrPile 100

DB 140428 CTGTATCTGACGACGCTCCCTCCCTGATTCACACTATCCAGTGGCGAAACTGATC 140487

OY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120

DB 140488 TTGGAGATTTCATGCTAGTATGCTTATCCGCTCAGCTTCATTCACCTGATATAGCAGC 140547

OY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSer 140

DB 140548 ATCCCTTCTCCTCACCCTGTTTCACACATCTCCGCTACGTGATGATCACCACCAAGAGC 140607

OY 141 CysPheSerIleHisTyrThrArgCysAlaValAlaLacysAlaValIleTyrPileIle 160

DB 140608 TGCTTTCCATTCACAAACCTGCATGAGTGTGAGCTGCTGCTGGTGGATCAT 140667

OY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180

DB 140668 TCCTGCTGAGCTGCTCATTCGGAAGACCTTCTTATCACAACAACAGAGCAGACAGCA 140727

OY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleTyrTyrAsnLeu 200

DB 140728 TCAGCTGCTGCACCTCAGCACTGCGATGGAATCATATCTTAAAGTGTGCAACCTG 140787

OY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220

DB 140788 ATTTGACTGCACACTACTTCTGCTCCCTGCTGATGATGACACTTGTCTATACACAG 140847

OY 221 IleTlleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240

DB 140848 ATTATCCACACTGTCACCCATGAGCAGCAAACTGACAGCTGCCCTTAAGCAGAAAGCAGCA 140907

OY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260

DB 140908 AGGCTAACCATTTGCTACTCCCTGCTGATTTTACGTATGTTTTTACCCTTCCATACCTTG 140967

OY 261 ArgValIleArgIleLeuSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280

DB 140968 AGGCTATTCGATGCAATCTCCCTGCTTCAATCAGTTGTTCCATGGAATGCAATGATC 141027

OY 281 HisGluAlaTyrTlleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300

DB 141028 CATTAGCTTACATCTTCTTCAACCATTAAGCTGCTGTAACACTTGGTAACTGTTTA 141087

OY 301 LeuTyrValIleValSerAspAsnPheGlnGlnAlaValCysSerThrValaGlyCysLys 320

DB 141088 CTTATATGCTGCTGCTGACCAAACTTTCAGCAGGCTGTCTGCTCAACAGTGAATGCAAA 141147

OY 321 ValSerGlyAsnLeuGlnAlaLysLysIleSerTyrSerAsnAsnPro 337

DB 141148 GTAAGGGAGACCTTGAGCAGCAAGAAATTAAGTACTCAAAACACCT 141198

RESULT 14

AX191332
LOCUS AX191332 1729 bp DNA linear PAR 15-AUG-2001
DEFINITION Sequence 2 from Patent WO0149847.
ACCESSION AX191332
VERSION AX191332.1 GI:15209582
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1729)
AUTHORS Glucksmann, M.A. and White, D.
TITLE 26904, 38911, and 39404, seven-transmembrane proteins / g-protein
JOURNAL coupled receptors
PATENT Patent: WO 0149847-A 2 12-JUL-2001;
Milenium Pharmaceuticals, Inc. (US)
FEATURES
source Location/Qualifiers
CDS
1..1729
/organism="Homo sapiens"
/db_xref="taxon:9606"
294..1307
/note="unnamed protein product"
/codon_start=1
/protein_id="GAC51133.1"
/db_xref="GI:15209583"
/translation="MNEPLDYLANSDPDDYAAFGNCTDENIPLMKHYLPVYGIIF
LVFPGNAVIVSYIFKMRPKSSTIMLACTDLYLSLPLHYVAGSNWJG
DFMKIRSEFHNLSILFLCFISFRCVTHHMSGSIKTKCAVACAVWII
SAVAIPMFELITSTNRTSACLOLSSDELMITKYNLITATFPCPLVITCY
TTIHTLTHLOQDSCLKOKARLTLLILATFVCLPPIIILVIRIBESLSSSI
ENQIHRAVIVSGPLALNFTGNLLTVVSDNFQAVSTVCKVSGNLEQARKISIS
NRP"
BASE COUNT 461 a 403 c 302 g 563 t
ORIGIN
Alignment Scores:
Pred. No.: 7.88e-126 Length: 1729
Score: 1764.00 Matches: 336
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.60% Indels: 0
DB: 6 Gaps: 0

US-10-023-775b-2 (1-337) x AX191332 (1-1729)

OY 1 MetAsnGluProLeuAspTyrLeuAlaAsnAlaSerAspPheProAspTyrAlaAla 20

DB 294 ATGAATGAGCCTAGACTATTTAGCAAAATGCTTCGATTTCCCGCATTAAGACGCT 353

OY 21 PheGlyAsnGlyThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40

DB 354 TTGGAAATGACCTGATGAAACATCCCAAGTGCAGTACCTCCCTGTTATTTAT 413

OY 41 GlyTllePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrTllePhe 60

DB 414 GGCAATATCTTCCTCGGGGATTTCCAGCAATGCAAGTATGATTCACATTTTC 473

OY 61 LysMetArgProThrLysSerSerThrIleIleMetLeuAsnIleuLacysThrAspLeu 80

DB 474 AAAATGAGACCTTGGAAAGACACACCATCATTTATGCTGAACCTGGCTGCACAGATCTG 533

OY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyGluAsnTyrPile 100

DB 534 CTGTATCTGACGACGCTCCCTCCCTGATTCACACTATCCAGTGGCGAAACTGATC 593

OY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120

DB 594 TTGGAGATTTCATGCTAGTATGCTTATCCGCTCAGCTTCATTCACCTGATATAGCAGC 653

OY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSer 140

DB 654 ATCCCTTCTCCTCACCCTGTTTCACACATCTTCGCTACTGCTGATCATTCACCAATGAGC 713

Human Cys79
Human G-protein cc
Human p21 purinoceptor
Novel
Human ATP receptor
Human ADP-like G
Human nGPCR #1.
Purinegic receptor
Purinegic receptor
Purinegic receptor
Turkey P2Y nucleoside
Gene 37 human secret
Human P2A receptor
Human P2Z pyrimidin
Human G-protein cc
Human G-protein cc
Human G-protein cc
Human G-protein cc
Human p2y-1 like gp
Human G-protein cc
Cysteinylyl leukotriene
Human LTR4 receptor
Human novel polypeptide
Human CysLW7-like
Human CysLW7-GPCR
Human G-protein cc
Human ADP-Like G
Human ATP receptor
Human g-protein cc
Human orphan G protein
Human G-protein cc
Human polypeptide

PR 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0203630.
 PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.

XX (AREN-) ARENA PHARM INC.

XX Chen R, Dang HT, Lowitz KP;

DR WPI; 2001-355616/37.
 DR N-PSDB; AAS07948.

PT Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -

PS Claim 53; Page 114-115; 160pp; English.

XX The sequence represents a human G-protein coupled receptor (GPCR),
 CC hRUP21. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilized to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.

XX Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 22; Length 337;
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPDIYLANASDPDYAAAFGNCNDENIPLMKHVLPVYGGIIFLVGPGNAVISTYIF 60
 DB 1 MNEPDIYLANASDPDYAAAFGNCNDENIPLMKHVLPVYGGIIFLVGPGNAVISTYIF 60
 QY 61 KMRPKMSSTIIMLNACTDLVLTSLPFLIHYYASGEMNIFGDFMCKFRFHFHNLYSS 120
 DB 61 KMRPKMSSTIIMLNACTDLVLTSLPFLIHYYASGEMNIFGDFMCKFRFHFHNLYSS 120
 QY 121 ILFLCFSTFRYCVIIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIMPTFLITSTNRNR 180
 DB 121 ILFLCFSTFRYCVIIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIMPTFLITSTNRNR 180
 QY 181 SACLDLTSSDELNTIKWNLITATTFCLPIVIVLCYTTIIHTLHGLQDSCCLKOKAR 240
 DB 181 SACLDLTSSDELNTIKWNLITATTFCLPIVIVLCYTTIIHTLHGLQDSCCLKOKAR 240
 QY 241 RLTIILLAFVYCFPLPHILRVIRIESRLSTISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
 DB 241 RLTIILLAFVYCFPLPHILRVIRIESRLSTISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
 QY 301 LYVVVSDNFQAVCGSTVRCKVSGNLEQAKKISYNNP 337
 DB 301 LYVVVSDNFQAVCGSTVRCKVSGNLEQAKKISYNNP 337

RESULT 2

ID AAO15399 standard; protein; 337 AA.

XX AAO15399;

DT 27-SEP-2002 (first entry)

1

DE Human G protein-coupled receptor.

XX Human; gene therapy; G protein-coupled receptor; drug development;
 KW central nervous system disease; endocrine disease; metabolic disease;
 KW cancer; respiratory disease; digestive disease; immune disease;
 KW inflammation; infection; circulatory disease.

OS Homo sapiens.

XX WO200257441-A1.

XX 25-JUL-2002.

PF 17-JAN-2002; 2002WO-JP00270.

PR 18-JAN-2001; 2001JP-0010714.

PR 30-MAR-2001; 2001JP-0102484.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Miwa M, Ito T, Shintani Y, Miyajima N;

DR WPI; 2002-566800/60.

DR N-PSDB; AAL43942.

PT Human kidney-originated G protein-coupled receptor protein TGR30 and
 PT encoded DNA, for developing drugs to treat central nervous diseases,
 PT endocrine diseases, metabolic diseases and cancer, including gene
 PT therapy

PS Claim 1; Page 88-90; 98pp; Japanese.

XX The invention comprises the amino acid and coding sequence of a human G
 CC protein-coupled receptor. The DNA and protein sequences of the invention
 CC are useful for developing drugs to prevent or treat (gene therapy):
 CC central nervous system diseases; endocrine diseases; metabolic diseases;
 CC cancer; respiratory diseases; digestive diseases; immune diseases;
 CC inflammations; infections; and circulatory diseases. The present amino
 CC acid sequence represents the human G protein-coupled receptor of the
 CC invention.

XX Sequence 337 AA;

Query Match 100.0%; Score 1771; DB 23; Length 337;
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEPDIYLANASDPDYAAAFGNCNDENIPLMKHVLPVYGGIIFLVGPGNAVISTYIF 60
 DB 1 MNEPDIYLANASDPDYAAAFGNCNDENIPLMKHVLPVYGGIIFLVGPGNAVISTYIF 60
 QY 61 KMRPKMSSTIIMLNACTDLVLTSLPFLIHYYASGEMNIFGDFMCKFRFHFHNLYSS 120
 DB 61 KMRPKMSSTIIMLNACTDLVLTSLPFLIHYYASGEMNIFGDFMCKFRFHFHNLYSS 120
 QY 121 ILFLCFSTFRYCVIIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIMPTFLITSTNRNR 180
 DB 121 ILFLCFSTFRYCVIIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIMPTFLITSTNRNR 180
 QY 181 SACLDLTSSDELNTIKWNLITATTFCLPIVIVLCYTTIIHTLHGLQDSCCLKOKAR 240
 DB 181 SACLDLTSSDELNTIKWNLITATTFCLPIVIVLCYTTIIHTLHGLQDSCCLKOKAR 240
 QY 241 RLTIILLAFVYCFPLPHILRVIRIESRLSTISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
 DB 241 RLTIILLAFVYCFPLPHILRVIRIESRLSTISCSIEHQIHEAYIVSRPLAALNTFGNLL 300
 QY 301 LYVVVSDNFQAVCGSTVRCKVSGNLEQAKKISYNNP 337
 DB 301 LYVVVSDNFQAVCGSTVRCKVSGNLEQAKKISYNNP 337

RESULT 3


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Db      241  |||
QY      301  LYYVSDNFQOAVCSTVRCKVSGNLEQAKKISYSNNP 337
          |||
Db      301  LYYVSDNFQOAVCSTVRCKVSGNLEQAKKISYSNNP 337
          |||

RESULT 4
ID      ABB83819 standard; Protein; 337 AA.
AC      ABB83819;
DT      18-SEP-2002 (first entry)
DE      Human P2Y-1like receptor variant SEQ ID NO 4.
KW      Human; P2Y-1like receptor; HIRPHM 0000037; immunity; inflammation;
KW      cancer; Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;
KW      immunomodulator; anti-inflammatory; cytostatic; antiasthmatic;
KW      gastrointestinal; anti-ulcer; antirheumatic; antiarthritic; virucide;
KW      antibacterial; immunosuppressive; dermatological; nephrotoxic;
KW      antiallergic; analgesic; receptor.
OS      Homo sapiens.
PN      GB2369364-A.
XX      29-MAY-2002.
PD      31-AUG-2001; 2001GB-0021215.
XX      01-SEP-2000; 2000GB-0021524.
XX      06-SEP-2000; 2000GB-0021894.
PR      25-SEP-2000; 2000GB-0023444.
XX      (GLAX ) GLAXO GROUP LTD.
PA      Foord SM, Ignar DM;
PI      WPI: 2002-511268/55.
XX      N-PSDB; ABN85630.
DR      An isolated P2Y-1like receptor polypeptide (HIRPHM 0000037) which can be
PT      used for the identification of agonists and antagonists which may be
PT      used to treat an immune or inflammatory disease -
PS      Claim 1; Page 30-31; 35pp; English.
XX      The invention relates to an isolated P2Y-1like receptor polypeptide
XX      (ABB83819-ABB83819) which is also referred to in the specification as
XX      HIRPHM 0000037. An effective amount of a substance (agonist or
XX      antagonist) which modulates P2Y receptor activity is useful to treat a
XX      subject having a disorder that is responsive to P2Y-1like receptor
XX      modulation. The disorder is a disease of immunity or inflammation. The
XX      substance may also be used to manufacture a medicine for the treatment or
XX      prophylaxis of a disorder that is responsive to stimulation or modulation
XX      of P2Y-1like receptor activity. Disorders which may be treated include
XX      colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,
XX      gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative
XX      colitis, rheumatoid arthritis, viral diseases, bacterial infections,
XX      autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic
XX      rhinitis, inflammatory pain and general inflammation such as tendonitis,
XX      polyostitis or prostatitis. The invention provides alternative
XX      substances for the treatment of immunological and inflammatory diseases.
XX      Sequence 337 AA:
XX
XX      Query Match 100.0%; Score 1771; DB 23; Length 337;
XX      Best Local Similarity 100.0%; Pred. No. 2,4e-194;
XX      Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

QY	1	MNPDLVYLNANSPEDPYAAAFGNCIDENIPKMHVLPVYIIFLVEGPGAAVYSYIF	60
Db	1	MNPEDVYLNANSPEDPYAAAFGNCIDENIPKMHVLPVYIIFLVEGPGAAVYSYIF	60
QY	61	KMPKPKSSITIMLNACTDLYLTSLPPLIHVYASGENWIFGDFMCKFIRSFHFNLSS	120
Db	61	KMPKPKSSITIMLNACTDLYLTSLPPLIHVYASGENWIGDFMCKFIRSFHFNLSS	120
QY	121	ILFLVCFISFRCAVLIHPMPCSFISIKRTCAVACAVWIIISLAVIPMTPLITSTNTR	180
Db	121	ILFLVCFISFRCAVLIHPMPCSFISIKRTCAVACAVWIIISLAVIPMTPLITSTNTR	180
QY	181	SACLDITSDELNTIKMYNLITATTFGLPLVYVLYCTTIIITHLTHGLQDSCLEKAR	240
Db	181	SACLDITSDELNTIKMYNLITATTFGLPLVYVLYCTTIIITHLTHGLQDSCLEKAR	240
QY	241	RLTILLLLAFYVCFEPHLLRVIRIESRLDISISCSIEHQIHEAVYVSPALALTFEGL	300
Db	241	RLTILLLLAFYVCFEPHLLRVIRIESRLDISISCSIEHQIHEAVYVSPALALTFEGL	300
QY	301	LYVYVSDNFOAVCSVRCKVSGNLEQAKKISYNNP	337
Db	301	LYVYVSDNFOAVCSVRCKVSGNLEQAKKISYNNP	337

CC	treatng conditions associated with an AXOR89 imbalance, such as
CC	bacterial, fungal or protozoan infections, cancers, pain, asthma,
CC	Parkinson's disease, diabetes, obesity, anorexia, bulimia, acute heart
CC	failure, hypotension, hypertension, urinary retention, osteoporosis,
CC	angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign
CC	prostatic hypertrophy, migraine, vomiting, psychotic, and neurological
CC	disorders, anxiety, schizophrenia, manic depression, delirium, dementia,
CC	dyskinesias, such as Huntington's Disease or Gilles de la Tourette's
CC	syndrome. The polynucleotide sequence may also be used for chromosome
CC	localisation or tissue expression studies. The AXOR89 is used as a
CC	vaccine or to produce fusion proteins. The present sequence is human
CC	AXOR89 protein.
xx	
xx	
SQ	Sequence 337 AA;
Query Match	100.0%; Score 1771; DB 23; Length 337;
Best Local Similarity	100.0%; Pred. NO. 2.4e-194;
Matches 337/	Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNPRLDYLANASDFPYAAAFGNCIDENPLKMHLPYIGIIFLVGPGNAVYSYIF	60
Db	1	MNPRLDYLANASDFPYAAAFGNCIDENPLKMHLPYIGIIFLVGPGNAVYSYIF	60
QY	61	KMRPKSSITIIIMNLACDLDLYISLPILHYASGENWITGDMCKFIRSFHNLYSS	120
Db	61	KMRPKSSITIIIMNLACDLDLYISLPILHYASGENWITGDMCKFIRSFHNLYSS	120
QY	121	ILFLTCFSIFRCVCIHHPMSCFSIHKTRCAVACAVWIIISLAVIIPMTFLITSTNTR	180
Db	121	ILFLTCFSIFRCVCIHHPMSCFSIHKTRCAVACAVWIIISLAVIIPMTFLITSTNTR	180
QY	121	ILFLTCFSIFRCVCIHHPMSCFSIHKTRCAVACAVWIIISLAVIIPMTFLITSTNTR	180
Db	121	ILFLTCFSIFRCVCIHHPMSCFSIHKTRCAVACAVWIIISLAVIIPMTFLITSTNTR	180
QY	181	SACLDITSSDELNTIKMYNLITATTFCLPLVYIYLCYTTIIHPLTHGLQDSCLOKKAR	240
Db	181	SACLDITSSDELNTIKMYNLITATTFCLPLVYIYLCYTTIIHPLTHGLQDSCLOKKAR	240
QY	241	RLTIILLILAFYVCFPHILRIYIRIESRLISISCSIEINOIHEAVYISRPILAALNTFENLL	300
Db	241	RLTIILLILAFYVCFPHILRIYIRIESRLISISCSIEINOIHEAVYISRPILAALNTFENLL	300
QY	301	LYVYVSDNFQOAVCSYVRCKVSGNLEQAKKISYSNNP	337
Db	301	LYVYVSDNFQOAVCSYVRCKVSGNLEQAKKISYSNNP	337

XX New human P2Y11 gene, useful for treatment and diagnosis of associated
 PT diseases, and related proteins, antibodies and modulators, encodes G
 PT protein-coupled receptor
 XX
 PS Claim 4; Page 3; 5pp; German.
 CC The invention relates to the human P2Y11 gene (1), including its 5' and
 CC 3' untranslated regions, located on chromosome 13 and encoding a G
 CC protein-coupled receptor. (1) and related mRNA, cDNA, protein, antibodies
 CC etc., are used for diagnosis and (gene) therapy of diseases that are
 CC (in)directly associated with (1) or its expression products. No diseases
 CC are specified but as (1) is expressed only in thyroid tissue, (1) is
 CC presumed to be involved in regulation of thyroid function. The present
 CC sequence is that of P2Y11.
 XX
 Q Sequence 337 AA:
 Query Match 100.0%; Score 1771; DB 23; Length 337;
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNEPLDYLANASDPDYAAAFGNGCTDENIPDKMNYLPVYIGIIFLVGFGPNNAVISTYIF 60
 DB 1 MNEPLDYLANASDPDYAAAFGNGCTDENIPDKMNYLPVYIGIIFLVGFGPNNAVISTYIF 60
 QY 61 KMPPKSSSTIMLNACTDLYLTLSPFLIHYYASGENMIFGDMCKEIRFSHFNYSS 120
 DB 61 KMPPKSSSTIMLNACTDLYLTLSPFLIHYYASGENMIFGDMCKEIRFSHFNYSS 120
 QY 121 ILFLTCFSIRYCVIIHPMSCFSIHKTRCAVAVCAVAVIISLVAVIPMTFLISTNRTNR 180
 DB 121 ILFLTCFSIRYCVIIHPMSCFSIHKTRCAVAVCAVAVIISLVAVIPMTFLISTNRTNR 180
 QY 181 SACLDTSSDELMTIKMYNLIATATPCPLVIVTLCYTTIIHTLHGLTDSCLKOKAR 240
 DB 181 SACLDTSSDELMTIKMYNLIATATPCPLVIVTLCYTTIIHTLHGLTDSCLKOKAR 240
 QY 241 RLTLILLAFYVCFPLPHILRVIRIESRLISCSISIEHQHEAVYSRPLAALNTFENL 300
 DB 241 RLTLILLAFYVCFPLPHILRVIRIESRLISCSISIEHQHEAVYSRPLAALNTFENL 300
 QY 301 LYYVSDNFOQAVCSYVRCKVSGNLEQAKKISTYNNP 337
 DB 301 LYYVSDNFOQAVCSYVRCKVSGNLEQAKKISTYNNP 337
 b
 RESULT 7
 AAU77600
 ID AAU77600 standard; Protein; 337 AA.
 XX
 AC AAU77600;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human P2Y1-like G protein-coupled receptor.
 XX
 KW Human; P2Y1-like G protein-coupled; receptor; GPCR;
 KW infection; pain; cancer; anorexia; bulimia; asthma; hypotension;
 KW central nervous system disease; acute heart failure; hypertension;
 KW urinary retention; osteoporosis; diabetes; angina pectoris;
 KW myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis;
 KW benign prostatic hypertrophy; psychosis; neurological disorder;
 KW dyskinnesia; HIV; human immunodeficiency virus infection; CNS disorder;
 KW Parkinson's disease; anxiety; schizophrenia; manic depression; delirium;
 KW dementia; severe mental retardation; Huntington's disease;
 KW Tourette's syndrome.
 XX
 OS Homo sapiens.
 XX
 PN W0200214511-A2.
 XX
 PD 21-FEB-2002.

XX
 PF 10-AUG-2001; 2001WO-EP09243.
 XX
 PR 14-AUG-2000; 2000US-224989P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Ramakrishnan S;
 XX
 DR WPI; 2002-257607/30.
 XX
 DR N-PSDB; ABK11381.
 PT Novel human P2Y1-like G protein-coupled receptor polypeptide which can
 PT be regulated for treating infection, pain, cancer, diabetes, anorexia,
 PT asthma, hypertension, neurological disorder and dyskinesia
 XX
 PS Claim 25; Fig 2; 118pp; English.
 XX
 CC The invention relates to a purified human P2Y1-like G protein-coupled
 CC receptor (GPCR) polypeptide and the nucleic acids encoding it
 CC (including 5' and 3' sequences, promoters, fragments, variants, or a
 CC sequence encoding a protein at least 50% identical to the GPCR).
 CC Also included are an expression vector comprising the nucleic acid,
 CC a host cell containing the vector and the identification of modulators of
 CC the GPCR especially those that reduce the activity of the GPCR.
 CC The nucleic acid is useful for detecting a polynucleotide encoding
 CC the GPCR in a biological sample. The GPCR and nucleic acid are useful for
 CC screening for agents which decrease the activity of the GPCR and
 CC for modulators of the GPCR. The modulator or agent useful for modulating
 CC the activity of P2Y1-like G protein-coupled receptor in a disease such as
 CC bacterial, fungal, protozoan, and viral infection, pain, cancer,
 CC anorexia, bulimia, asthma, central nervous system (CNS) disease, acute
 CC heart failure, hypotension, hypertension, urinary retention, ulcer,
 CC osteoporosis, diabetes, angina pectoris, myocardial infarction, ulcer,
 CC inflammation, allergy, multiple sclerosis, benign prostatic hypertrophy,
 CC psychotic and neurological disorders, dyskinesias, HIV virus infection
 CC (human immunodeficiency virus), CNS disorders such as Parkinson's
 CC disease, anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation, Huntington's disease and Tourette's syndrome.
 CC The present sequence represents the P2Y1-like GPCR of the invention.
 XX
 SQ Sequence 337 AA:
 Query Match 100.0%; Score 1771; DB 23; Length 337;
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;
 Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNEPLDYLANASDPDYAAAFGNGCTDENIPDKMNYLPVYIGIIFLVGFGPNNAVISTYIF 60
 DB 1 MNEPLDYLANASDPDYAAAFGNGCTDENIPDKMNYLPVYIGIIFLVGFGPNNAVISTYIF 60
 QY 61 KMPPKSSSTIMLNACTDLYLTLSPFLIHYYASGENMIFGDMCKEIRFSHFNYSS 120
 DB 61 KMPPKSSSTIMLNACTDLYLTLSPFLIHYYASGENMIFGDMCKEIRFSHFNYSS 120
 QY 121 ILFLTCFSIRYCVIIHPMSCFSIHKTRCAVAVCAVAVIISLVAVIPMTFLISTNRTNR 180
 DB 121 ILFLTCFSIRYCVIIHPMSCFSIHKTRCAVAVCAVAVIISLVAVIPMTFLISTNRTNR 180
 QY 181 SACLDTSSDELMTIKMYNLIATATPCPLVIVTLCYTTIIHTLHGLTDSCLKOKAR 240
 DB 181 SACLDTSSDELMTIKMYNLIATATPCPLVIVTLCYTTIIHTLHGLTDSCLKOKAR 240
 QY 241 RLTLILLAFYVCFPLPHILRVIRIESRLISCSISIEHQHEAVYSRPLAALNTFENL 300
 DB 241 RLTLILLAFYVCFPLPHILRVIRIESRLISCSISIEHQHEAVYSRPLAALNTFENL 300
 QY 301 LYYVSDNFOQAVCSYVRCKVSGNLEQAKKISTYNNP 337
 DB 301 LYYVSDNFOQAVCSYVRCKVSGNLEQAKKISTYNNP 337
 RESULT 8

XX The invention relates to human G-protein coupled receptor (GqREC).
 CC polypeptides and polynucleotides. GqREC polypeptides are useful for
 CC screening compounds that modulate their activity. They are useful in
 CC the diagnosis, prevention and treatment of disorders which include
 CC cell proliferative disorders such as arteriosclerosis, hepatitis,
 CC myeloidbrosis, psoriasis and cancer including adenocarcinoma, leukaemia,
 CC lymphoma; neurological disorders such as epilepsy, ischaemic
 CC cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia,
 CC Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral
 CC meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia
 CC cardiovascular disorders such as arteriovenous fistula, atherosclerosis,
 CC hypertension, vascular tumours, myocardial infarction, hypertensive
 CC heart disease, infective endocarditis, cardiomyopathy, myocarditis;
 CC gastrointestinal disorders such as dysphagia, peptic oesophagitis,
 CC emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea,
 CC constipation, acquired immune deficiency syndrome (AIDS), hepatic
 CC encephalopathy; autoimmune/inflammatory disorders such as Addison's
 CC disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact
 CC dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome,
 CC emphysema, Grave's disease, gout, multiple sclerosis, Rheumatoid
 CC arthritis, systemic lupus erythematosus, uveitis, viral, bacterial,
 CC fungal, parasitic, protozoal and helminthic infections and trauma;
 CC metabolic disorders such as diabetes, obesity and osteoporosis; and
 CC viral infections such as infection caused by viral agent classified as
 CC adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention
 CC are useful as probes for assessing toxicity of test compounds. They are
 CC also used in gene therapy. The present sequence is human G-protein
 CC coupled receptor 2 (GqREC-2) protein.

SQ Sequence 337 AA;

Query Match	100.0%;	Score 1771;	DB 23;	Length 337;
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Best Local Similarity 100.0%; Pred. No. 2.4e-194;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy	1	MNPDLIYANASDFP	YAAAFGNC	NDENIPLK	MHLPYIGIIF	YVGP	GAAYIS	YIF	60
Qy	2	MNPDLIYANASDFP	YAAAFGNC	NDENIPLK	MHLPYIGIIF	YVGP	GAAYIS	YIF	60
Dd	1	MNPDLIYANASDFP	YAAAFGNC	NDENIPLK	MHLPYIGIIF	YVGP	GAAYIS	YIF	60
Qy	61	KMPKMSSTIIMLN	ACTDLYLTSLP	LIHYASG	ENWITG	DMCKFIR	SFHN	YSS	120
Dd	61	KMPKMSSTIIMLN	ACTDLYLTSLP	LIHYASG	ENWITG	DMCKFIR	SFHN	YSS	120
Y	121	ILELFGFSIFRCV	IIHPMSCFI	HKTRCAV	AVACVWIIISL	VAVIPMT	FLITS	NTNR	180
Dd	121	ILELFGFSIFRCV	IIHPMSCFI	HKTRCAV	AVACVWIIISL	VAVIPMT	FLITS	NTNR	180
Y	121	ILELFGFSIFRCV	IIHPMSCFI	HKTRCAV	AVACVWIIISL	VAVIPMT	FLITS	NTNR	180
Dd	121	ILELFGFSIFRCV	IIHPMSCFI	HKTRCAV	AVACVWIIISL	VAVIPMT	FLITS	NTNR	180
Qy	181	SACLDITSSDE	LNTIKWNLIT	ATPFCPL	YIVYVLCY	TTIIH	TLHGL	QDSC	240
Dd	181	SACLDITSSDE	LNTIKWNLIT	ATPFCPL	YIVYVLCY	TTIIH	TLHGL	QDSC	240
Y	181	SACLDITSSDE	LNTIKWNLIT	ATPFCPL	YIVYVLCY	TTIIH	TLHGL	QDSC	240
Dd	181	SACLDITSSDE	LNTIKWNLIT	ATPFCPL	YIVYVLCY	TTIIH	TLHGL	QDSC	240
Qy	241	RLTILLLAFY	CVFPHIL	IRVIRIES	RLSISCSIE	NOIHEAV	IVSRPL	LAAL	300
Dd	241	RLTILLLAFY	CVFPHIL	IRVIRIES	RLSISCSIE	NOIHEAV	IVSRPL	LAAL	300
Y	241	RLTILLLAFY	CVFPHIL	IRVIRIES	RLSISCSIE	NOIHEAV	IVSRPL	LAAL	300
Dd	241	RLTILLLAFY	CVFPHIL	IRVIRIES	RLSISCSIE	NOIHEAV	IVSRPL	LAAL	300
Qy	301	LYVYVSDNFQ	AAVCSVTR	CKSGNLE	QAOKKIS	YSNP	337		
Dd	301	LYVYVSDNFQ	AAVCSVTR	CKSGNLE	QAOKKIS	YSNP	337		
Y	301	LYVYVSDNFQ	AAVCSVTR	CKSGNLE	QAOKKIS	YSNP	337		
Dd	301	LYVYVSDNFQ	AAVCSVTR	CKSGNLE	QAOKKIS	YSNP	337		

RESULT 10

ID AU04584 standard; Protein; 337 AA.

AC AAU04584;

DT 26-SEP-2001 (first entry)

DE Human G-protein coupled receptor, GPCR 39404.

KW Human; G-protein coupled receptor; GPCR; 39404; 1immunogen; antibody;

·KW Good pasture's syndrome; viral hepatitis; Alzheimer's disease; lymphoma;

KW Heymann nephritis; Paget's disease; Crohn's disease; endometriosis
KW Systemic lupus erythematosus; actinic keratosis; myocarditis;
KW Kawasaki syndrome; Digeorge syndrome; peripheral B-cell neoplasm;
KW inflammations; teratoma.

OS Homo sapiens.

FH	Key	Location/Qualifiers
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
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88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

/label = Biologically_active_peptide

PN WO200149847-A2

PD 12-JUL-2001

PF 22-DEC-2000; 2000WO-US35309

PR 30-DEC-1999; 99US-0475790.

PA (MILL-) MILLENNIUM PHARM INC.

PI Glucksmann MA, White D;

DR WPI; 2001-432880/46.

DR N-PSDB; AAS08362.

PT Novel isolated 26904, 38911 and 39404 polypeptides which are seven transmembrane proteins belonging to superfamily of G-protein-coupled PT receptors, useful for treating disorders of spleen, lung, liver, brain PT and kidney -

PS Claim 8; Fig 1; 164pp; English

The sequence represents a novel human seven transmembrane domain protein belonging to the G-protein coupled receptor (GPCR) superfamily, protein 39404. The receptor is useful in drug screening assays, to identify compounds that modulate receptor activity and/or interact with the receptor, and for producing antibodies specific for the receptor, its regions or fragments. The receptor is useful for treating/diagnosing a 26904, 39911 and 39404 protein-associated disorder characterised by aberrant expression or activity of the protein, for monitoring therapeutic effect during clinical trials and other treatment, as bait proteins in a two-hybrid or three-hybrid assay, and in pharmacogenomic analysis. The proteins and nucleic acids encoding them are useful for diagnosis and treatment of disorders selected from disorders of the spleen, lung such as Good pasture's syndrome, liver such as viral hepatitis, brain such as Alzheimer's disease, haematopoietic stem cells such as lymphoma, kidney such as Heymann nephritis, bone such as Paget's disease, colon such as Crohn's disease, uterus and endometrium such as endometriosis, T-cell disorders such as systemic lupus erythematosus, diseases of the skin such as actinic keratosis, disorders of the heart such as myocarditis, disorders involving blood vessels such as Kawasaki syndrome, disorders involving the thymus such as DiGeorge syndrome, disorders involving B-cells such as peripheral B-cell neoplasms, disorders of the breast such as inflammations, and disorders involving the testis and epididymis such as tetraoma. Numerous examples of each type of disorder are given in the specification.

SQ Sequence 337 AA;

Best Local Similarity 99.78; Pred. No. 1.5e-193;

[illegible]

	Qy	Db	Qy	Db	Qy
	1	1	61	61	121
	MNPELDYLANASDFPDYAAAFGNCNDENPLKMHLPYIYGIIFVGPAGNAVISTYIE	MNPELDYLANASDFPDYAAAFGNCNDENPLKMHLPYIYGIIFVGPAGNAVISTYIE	KMPKMSSTIMLNACTDGLTSLPILIHVYASGEMWIGDGMCKFIRSPSEFENLYSS	KMPKMSSTIMLNACTDGLTSLPILIHVYASGEMWIGDGMCKFIRSPSEFENLYSS	ILFLVCFISFRVCVLIHPMSCFSEIHKTRCAAVACAAVMIISLVAVIIPTELTISTNFTNR
	60	60	120	120	180
	1	1	61	61	121
	MNPELDYLANASDFPDYAAAFGNCNDENPLKMHLPYIYGIIFVGPAGNAVISTYIE	MNPELDYLANASDFPDYAAAFGNCNDENPLKMHLPYIYGIIFVGPAGNAVISTYIE	KMPKMSSTIMLNACTDGLTSLPILIHVYASGEMWIGDGMCKFIRSPSEFENLYSS	KMPKMSSTIMLNACTDGLTSLPILIHVYASGEMWIGDGMCKFIRSPSEFENLYSS	ILFLVCFISFRVCVLIHPMSCFSEIHKTRCAAVACAAVMIISLVAVIIPTELTISTNFTNR
	60	60	120	120	180

```

Db      121 ILELTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLTSTNRTNR 180
Oy      181 SACLDTSSDELNTIKMYNLIATATFCPLVIVTLCYTTIHTLHGLOTDSCLQOKAR 240
Db      181 SACLDTSSDELNTIKMYNLIATATFCPLVIVTLCYTTIHTLHGLOTDSCLQOKAR 240
Oy      241 RTILLLLAFFVYCFELPHILRVIRISRLISCSISCIENQIHEAVIYSRPLAALNTFENL 300
Db      241 RTILLLLAFFVYCFELPHILRVIRISRLISCSISCIENQIHEAVIYSRPLAALNTFENL 300
Oy      301 LYYVSDNFOQAVCSTVRCKVSGNLEQAKKISYSNP 337
Db      301 LYYVSDNFOQAVCSTVRCKVSGNLEQAKKISYSNP 337
Db      301 LYYVSDNFOQAVCSTVRCKVSGNLEQAKKISYSNP 337

RESULT 11
AAG80971
ID      AAG80971 standard; Protein; 336 AA.
AC      AAG80971;
XX      28-AUG-2001 (first entry)
DT      Human nGPCR54 #2.
XX      G protein-coupled receptor; nGPCR; seven transmembrane receptor;
KM      signal transduction; schizophrenia; thyroid disorder; renal failure;
KM      rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KM      cardiovascular disease; proliferative disorder; hormonal disorder;
KM      neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KM      attention deficit-hyperactivity disorder/attention deficit disorder;
KM      Parkinson's disease; migraine; senile dementia; inflammatory disease;
KM      rheumatoid arthritis; autoimmune disorder; respiratory ailment;
KM      neuroprotective.
XX      Homo sapiens.
OS      Homo sapiens.
XX      WO200136473-A2.
XX      25-MAY-2001.
XX      16-NOV-2000; 2000MO-US31581.
XX      16-NOV-1999; 99US-0165838.
XX      17-NOV-1999; 99US-0166071.
XX      19-NOV-1999; 99US-0166678.
XX      28-DEC-1999; 99US-0173396.
XX      22-FEB-2000; 2000US-0184129.
XX      28-FEB-2000; 2000US-0185421.
XX      28-FEB-2000; 2000US-0185554.
XX      02-MAR-2000; 2000US-0186530.
XX      03-MAR-2000; 2000US-0186811.
XX      09-MAR-2000; 2000US-0188114.
XX      17-MAR-2000; 2000US-0190310.
XX      21-MAR-2000; 2000US-0190800.
XX      20-APR-2000; 2000US-0198568.
XX      02-MAY-2000; 2000US-0201190.
XX      08-MAY-2000; 2000US-0203111.
XX      25-MAY-2000; 2000US-0207094.
XX      (PHAA ) PHARMACIA & UPJOHN CO.
XX      Vogeli G, Wood LS, Parodi LA, Hiesbach RR, Lind P, Slightom J;
PI      Schellin KA, Kayes PS, Bannigan CM, Ruff V, Sejlitz T, Ruff RM;
XX      WPI; 2001-389626/41.
XX      N-PSDB; AAH51011.
XX      New G protein-coupled receptor (nGPCR-x) and its encoding
PT      polynucleotide useful for diagnosing and treating e.g. schizophrenia -
XX      Claim 37; Page 91; 261pp; English.

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XX      The present invention relates to novel G protein-coupled receptors
CC      (nGPCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
CC      28, 31-38, 40, 41, 53-60) and their coding sequences. The present
CC      sequence is one such G protein-coupled receptor. GPCRs are also known as
CC      seven transmembrane receptors and function in signal transduction. The
CC      nGPCR coding sequences are useful for screening a human to diagnose a
CC      disorder affecting the brain or a genetic predisposition, specifically
CC      schizophrenia. nGPCR are useful for identifying compounds useful for
CC      treating schizophrenia. Detection of nGPCR in a sample is useful as a
CC      diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
CC      failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
CC      metabolic and cardiovascular diseases, proliferative disorders and
CC      hormonal disorders. Modulators of nGPCR activity have the utility for
CC      treating neurological disorders, including schizophrenia, ADHD/ADD
CC      (attention deficit-hyperactivity disorder/attention deficit disorder),
CC      and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
CC      migraine and senile dementia. Additional disorders include inflammatory
CC      conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
CC      disorders, cancers, respiratory ailments such as asthma, and inflammatory
CC      diseases e.g. inflammatory bowel disease.
XX      Sequence 336 AA:
SQ      Query Match 90.5%; Score 1602.5; DB 22; Length 336;
        Best Local Similarity 92.0%; Pred. No. 5.1e-175;
        Matches 312; Conservative 6; Mismatches 14; Indels 7; Gaps 3;
Oy      1 MNEPLDYLANASFPDYAAAFGCTDENTIPKMHYIPVYIGTIFLVGFGNNAVISTYTF 60
Db      1 MNEPLDYLANASFPDYAAAFGCTDENTIPKMHYIPVYIGTIFLVGFGNNAVISTYTF 60
Oy      61 KMRPKSSTIIMNLACTDLYLTSPLFIHYVASEGNTFGDMKFTFHSFHFMYSS 120
Db      61 KMRPKSSTIIMNLACTDLYLTSPLFIHYVASEGNTFGDMKFTFHSFHFMYSS 120
Oy      121 ILELTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLTSTNRTNR 180
Db      121 ILELTCFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLTSTNRTNR 180
Oy      181 SACLDTSSDELNTIKMYNLIATATFCPLVIVTLCYTTIHTLHGLOTDSCLQOKAR 240
Db      181 SACLDTSSDELNTIKMYNLIATATFCPLVIVTLCYTTIHTLHGLOTDSCLQOKAR 240
Oy      241 RTILLLLAFFVYCFELPHILRVIRISRLISCSISCIENQIHEAVIYSRPLAALNTF 296
Db      241 RTILLLLAFFVYCFELPHILRVIRISRLISCSISCIENQIHEAVIYSRPLAALNTF 297
Oy      297 GNLLLYVVSDFNQAVCSTVRCKVSGNLEQAKKISYSN 335
Db      298 GNLLLYVVSDFNQAVCSTVRCKVSGNLEQAKKISYSN 336

RESULT 12
ABB83818
ID      ABB83818 standard; Protein; 276 AA.
AC      ABB83818;
XX      18-SEP-2002 (first entry)
DT      Human P2Y-1like receptor SEQ ID NO. 2.
XX      Human P2Y-1like receptor SEQ ID NO. 2.
XX      Human: P2Y-1like receptor; HIPHM 0000037; immunity; inflammation;
DE      cancer; Crohn's disease; irritable bowel syndrome; rheumatoid arthritis;
XX      immunomodulator; anti-inflammatory; cytostatic; antiscumatic;
XX      gastrointestinal; anti-ulcer; antirheumatic; antiarthritic; virocidic;
XX      antibacterial; immunosuppressive; dermatological; nephrotropic;
XX      antiallergic; analgesic; receptor.
OS      Homo sapiens.
XX      GB2369364-A.
XX      GB2369364-A.

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[illegible]

XX		Human protein SEQ ID NO 1959.
DE		
XX		Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW		vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM		tissue growth factor; immunomodulatory; cancer; leukaemia;
KX		nervous system disorder; arthritis; inflammation.
XX		
OS	Homo sapiens.	
XX		
PN	MO200157190-A2.	
PD	09- AUG -2001.	
PF	05-FEB -2001; 2001WO-US04098.	
XX		
PR	03-FEB -2000; 2000US-0496914.	
PR	27-APR -2000; 2000US-0560875.	
PR	20-JUN -2000; 2000US-0596075.	
PR	19-JUL -2000; 2000US-0620325.	
PR	01-SEP -2000; 2000US-0654936.	
PR	15-SEP -2000; 2000US-0663561.	
PR	20-OCT -2000; 2000US-0693325.	
PR	30-NOV -2000; 2000US-0728422.	
XX		
PA	(HYSE-) HYSE INC.	
PI	Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Gao Y, Ma Y;	
PI	Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZM;	
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;	
DR	WPI: 2001-476283/51.	
XX	N-PSDB; AAK52430.	
PT		
NU	Nucleic acids encoding polypeptides with cytokine-like activities,	
US	useful in diagnosis and gene therapy -	
XX		
PS	Claim 20; Page 4370-4371; 6221pp; English.	
XX		
CC	The invention relates to polynucleotides (AAK51456-AAK53435) and the	
CC	encoded polypeptides (AAM78323-AAH80302) that exhibit activity elating to	
CC	cytokine, cell proliferation or cell differentiation or which may induce	
CC	production of other cytokines in other cell populations. The	
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or	
CC	peptide therapy. The polypeptides have various cytokine-like activities,	
CC	e.g. stem cell growth factor activity, haematopoiesis regulating	
CC	activity, tissue growth factor activity, immunomodulatory activity and	
CC	activity/inhibitin activity and may be useful in the diagnosis and/or	
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and	
CC	inflammation.	
CC	Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666	
CC	(AAH80020) are omitted as the relevant pages from the sequence listing	
CC	were missing at the time of publication.	
SQ	Sequence 230 AA:	
Query Match	62.2%; Score 1102; DB 22; Length 230;	
Best Local Similarity	100.0%; Pred. No. 8e-118;	
Matches	206; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
D6	1 MNEPLDYLANASDPFYAARFNGCNDENIPLKMHYLPVIYGIIFLVGPGNAVVISTYLE 60	
OY	1 MNEPLDYLANASDPFYAARFNGCNDENIPLKMHYLPVIYGIIFLVGPGNAVVISTYLE 60	
D6	61 KMRPKSKSTIIIMLNACTDLDLYTSLPFLIHYYAGGEWMINGDFCKIRFSFHNLXS 120	
OY	61 KMRPKSKSTIIIMLNACTDLDLYTSLPFLIHYYAGGEWMINGDFCKIRFSFHNLXS 120	
D6	121 ILFTLCGFIFRCYCVIIHPMSCFSIKTKTCAYAVACAVVMIIISLVAVIPMTFLTSTNNRTNR 180	
OY	121 ILFTLCGFIFRCYCVIIHPMSCFSIKTKTCAYAVACAVVMIIISLVAVIPMTFLTSTNNRTNR 180	
DB	121 ILFTLCGFIFRCYCVIIHPMSCFSIKTKTCAYAVACAVVMIIISLVAVIPMTFLTSTNNRTNR 180	
OY	181 SAGCIDLTSSDELNTIKMYNLILTATTT 206	

Db 181 SACLDTSSDELNTIKMYNLTRAT 206

|||||

RESULT 14

ABBI1082

ID ABBI1082 standard; peptide; 179 AA.

XX

AC ABBI1082;

XX

DT 11-JAN-2002 (first entry)

XX

DE Human P2Y purinoceptor homologue, SEQ ID NO:1452.

XX

KM Human; cytokine; cell proliferation; cell differentiation; growth factor;

KM haematopoiesis regulation; tissue growth; immunomodulator; activin;

KM inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;

KM proliferation; metastasis; cancer; tumour; haematopoietic disorder;

KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

KM chronic inflammatory condition; proliferative retinopathy;

KM atherosclerosis; coronary heart disease; arterial ischaemia;

KM bone disorder; osteoporosis; vascular growth disorder;

KM tissue regeneration; wound healing; infection; immune disorder;

KM cell culture; drug screening; gene therapy; antiinflammatory;

KM antiasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;

KM cytoskeletal; osteopathic; vasotropic; cardiant; virucide; antibacterial;

KM antifungal; vulnery; antiulcer.

XX

OS Homo sapiens.

XX

PN W0200157188-A2.

XX

PD 09-AUG-2001.

XX

PE 05-FEB-2001; 2001WO-US03800.

XX

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

XX

XX (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-457740/49.

DR N-PSDB; ABA08326.

XX

PT Human proteins and DNA encoding sequences useful for preventing,

PT treating or ameliorating a medical condition in a mammalian subject

PT e.g. arthritis and cancer -

XX

PS Claim 20; Page 144; 1963pp; English.

XX

XX Sequences ABBI0981-ABBI12330 represent 1350 novel human polypeptides, and

XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The

XX invention also relates to vectors and recombinant host cells comprising a

XX nucleotide of the invention, methods of producing the novel polypeptides,

XX antibodies against the polypeptides, methods of detecting the nucleotides

XX or polypeptides in a sample, and methods of identifying compounds which

XX bind to polypeptides of the invention. Although novel, many of the

XX polypeptides of the invention have homology to known proteins, thereby

XX giving an insight into their probable biological activities, and hence

XX potential therapeutic applications. The polypeptides of the invention may

XX have various activities, including cytokine, cell proliferation or cell

XX differentiation activities; stem cell growth factor activity;

XX haematopoiesis regulatory activity; tissue growth activity;

XX immunomodulatory activity; activin- or inhibin-related activities;

XX chemotactic or chemokinetic activities; haemostatic, thrombotic or

XX thrombolytic activities; receptor or ligand activities; or may be

XX involved in oncogenesis, cancer cell proliferation or metastasis.

XX Depending on their biological activities, polypeptides and nucleotides of

XX the invention are useful for preventing, treating or ameliorating medical

XX conditions, e.g., by protein or gene therapy. Such conditions include

XX cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

CC proliferative retinopathy, atherosclerosis, coronary heart disease,

CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with

CC immunomodulatory activities may be used in the treatment of viral,

CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to

CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness,

CC autoimmune disease or accidental damage. The polypeptides and nucleotides

CC may also be used in the diagnosis of the above conditions, and in drug

CC screening techniques. The present sequence represents a novel human

CC polypeptide of the invention.

XX

XX Sequence 179 AA;

XX

XX Query Match 49.8%; Score 881.5; DB 22; Length 179;

XX Best Local Similarity 94.9%; Pred. No. 1.1e-92;

XX Matches 169; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

XX

QY 70 TMLNACDPLVLTSLPFIHNYASGEMNIFGDFMCKFRFSFHEMLYSIIFLCFSI 129

Db 3 LLMNLALMDPLVLTSLPFIHNYASGEMNIFGDFMCKFRFSFHEMLYSIIFLCFSI 62

QY 130 FRCVTHPMSCFSIHTRCAVAVCAVWIIISLVAVIPMFELTSTRTRRSACLDITSS 189

Db 63 FRCVTHPMSCFSIHTRCAVAVCAVWIIISLVAVIPMFELTSTRTRRSACLDITSS 122

QY 190 DELNTIKMYNLITATFCEPLVIVTLCYTTIITHTLHNGIOTPSCLKQKARRLITILL 247

Db 123 DELNTIKMYNLITLA-LLCPLVIVTLCYTTIITHTLHNGHANSCLKQKARRLITILL 179

XX

XX RESULT 15

XX AAM80281

XX ID AAM80281 standard; Protein; 179 AA.

XX

XX AAM80281;

XX

XX 06-NOV-2001 (first entry)

XX

XX Human protein seq ID NO 3927.

XX

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;

XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

XX tissue growth factor; immunomodulatory; cancer; leukaemia;

XX nervous system disorder; arthritis; inflammation.

XX

XX Homo sapiens.

XX

XX W0200157190-A2.

XX

XX 09-AUG-2001.

XX

XX 05-FEB-2001; 2001WO-US04098.

XX

XX 03-FEB-2000; 2000US-0496914.

XX 27-APR-2000; 2000US-0560875.

XX 20-JUN-2000; 2000US-0598075.

XX 19-JUL-2000; 2000US-0620325.

XX 01-SEP-2000; 2000US-0654936.

XX 15-SEP-2000; 2000US-0663561.

XX 20-OCT-2000; 2000US-0693325.

XX 30-NOV-2000; 2000US-0728422.

XX

XX (HYSE-) HYSEQ INC.

XX

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Gao Y, Ma Y;

XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

XX Xue AD, Yang Y, Wejhtman T, Goodrich R;

XX WPI: 2001-476283/51.
 DR N-PSDB; AAK53414.

XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX

PS Claim 20: Page 470; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAK/8323-AAK80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibitor activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAK80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX

Sequence 179 AA;

Query Match 49.8%; Score 881.5; DB 22; Length 179;
 Best Local Similarity 94.9%; Pred. No. 1.1e-92;
 Matches 169; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 70 IIMLNACTDLYLTLSPFLIHYASGEMIFGDMCKFIRFSFHNLYSSILFNCFSI 129
 :::
 Db 3 LLMNLALDLYLTLSPFLIHYASGEMIFGDMCKFIRFSFHNLYSSILFNCFSI 62
 QY 130 FRVCYIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLITSNRTNRSACDLTSS 189
 :::
 Db 63 FRVCYIIHPMSCFSIHKTRCAVAVCAVWIIISLVAVIPMTFLITSNRTNRSACDLTSS 122
 QY 190 DELNTIKWYNLITATFPLPLIVIVLCTTIIHTLHGLQTSCLKOKARRLTILL 247
 :::
 Db 123 DELNTIKWYNLITA-LTCLPLIVIVLCTTIIHTLHGLHANSCLKOKARRLTILL 179

Search completed: May 30, 2003, 13:44:36
 Job time : 72 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 13:44:43 ; Search time 21 Seconds
(without alignments)
1624.399 Million cell updates/sec

Title: US-10-023-775b-2
Perfect score: 1771
Sequence: 1 MNEPLDYLANASDPDYAA.....RCKVSGNLBOAKISYNNP 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the chance being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1771	100.0	337	9	US-10-023-775b-2
2	1771	100.0	337	9	US-10-270-144-2
3	1771	100.0	337	9	US-10-188-405-8
4	1771	100.0	337	9	US-09-885-453-1
5	1771	100.0	337	10	US-09-943-798-4
6	1602.5	90.5	336	9	US-09-782-974C-86
7	1444	81.5	276	10	US-09-943-798-2
8	831.5	47.0	192	9	US-09-782-974C-60
9	575	32.5	299	9	US-10-270-144-4
10	567	32.0	373	9	US-10-092-135-6
11	565.5	31.9	362	9	US-10-092-135-3
12	565.5	31.9	362	9	US-10-092-135-4
13	565.5	31.9	362	9	US-09-779-679-28
14	565	31.9	373	9	US-10-092-135-7
15	562	31.7	365	9	US-10-092-135-5
16	514	29.0	355	9	US-09-077-173A-2
17	488	27.6	334	9	US-10-270-587-2
18	487.5	27.5	330	10	US-09-826-791-2
19	487.5	27.5	346	9	US-09-828-478-2

20	487.5	27.5	346	9	US-09-779-679-2	Sequence 2, Appl1
21	487.5	27.5	346	9	US-09-779-679-26	Sequence 26, Appl1
22	487.5	27.5	346	10	US-09-826-791-6	Sequence 6, Appl1
23	487.5	27.5	346	10	US-09-866-230-7	Sequence 7, Appl1
24	487.5	27.5	346	10	US-09-866-230-9	Sequence 9, Appl1
25	479	27.0	341	9	US-10-270-587-3	Sequence 3, Appl1
26	477	26.9	334	10	US-09-765-034-2	Sequence 2, Appl1
27	426	24.1	317	9	US-09-881-138A-2	Sequence 2, Appl1
28	397	22.4	357	9	US-09-966-755-2	Sequence 2, Appl1
29	397	22.4	357	10	US-09-903-377-2	Sequence 2, Appl1
30	397	22.4	357	10	US-09-952-385-2	Sequence 2, Appl1
31	397	22.4	357	12	US-10-000-759A-2	Sequence 2, Appl1
32	394.5	22.3	339	9	US-09-828-478-4	Sequence 4, Appl1
33	394.5	22.3	339	10	US-09-848-889-12	Sequence 12, Appl1
34	394.5	22.3	339	10	US-09-788-133-2	Sequence 2, Appl1
35	394.5	22.3	367	9	US-09-828-478-6	Sequence 6, Appl1
36	388.5	21.9	425	10	US-09-782-980-80	Sequence 80, Appl1
37	388.5	21.9	425	10	US-09-884-430-4	Sequence 4, Appl1
38	380	21.5	356	9	US-09-779-679-25	Sequence 25, Appl1
39	379.5	21.4	338	9	US-09-885-453-4	Sequence 4, Appl1
40	375.5	21.2	359	9	US-10-094-417-10	Sequence 10, Appl1
41	375.5	21.2	359	9	US-09-782-974C-76	Sequence 76, Appl1
42	375.5	21.2	359	10	US-09-739-151-2	Sequence 2, Appl1
43	372	20.9	302	9	US-10-024-694-30	Sequence 30, Appl1
44	371	20.9	332	9	US-10-001-835-140	Sequence 140, Appl1
45	371	20.9	348	10	US-09-827-937A-17	Sequence 17, Appl1

ALIGNMENTS

RESULT 1
US-10-023-775b-2
Sequence 2, Application US/10023775b
Publication No. US2003002282A1
GENERAL INFORMATION:
APPLICANT: Pfizer Ltd. (EP/GB only)
APPLICANT: Pfizer Inc. (US, JP, EB except GB)
APPLICANT: Fidock, Mark David
TITLE OR INVENTION: No. US2003002282A1 Polypeptide
FILE REFERENCE: PCI0959AGPR
CURRENT APPLICATION NUMBER: US/10/023, 775b
CURRENT FILING DATE: 2001-12-18
PRIORITY APPLICATION NUMBER: GB 0030854.4
PRIORITY FILING DATE: 2000-12-18
PRIORITY APPLICATION NUMBER: US 60/260,590
PRIORITY FILING DATE: 2001-01-09
PRIORITY APPLICATION NUMBER: US 60/296,660
PRIORITY FILING DATE: 2001-06-07
PRIORITY APPLICATION NUMBER: GB 0111031.1
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 337
TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-775b-2
Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3, 2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNEPLDYLANASDPDYAAAFGKCTDENTDLKMHYLPVYIGIIFLVGFPNNAYISTYIF 60
DB 1 MNEPLDYLANASDPDYAAAFGKCTDENTDLKMHYLPVYIGIIFLVGFPNNAYISTYIF 60
QY 61 KMPPKWSSTIMLNACTDLYLTSUPELHHYASGNNTEFGPMCKFIRESHPNYSX 120
DB 61 KMPPKWSSTIMLNACTDLYLTSUPELHHYASGNNTEFGPMCKFIRESHPNYSX 120
QY 121 ILFLTFISIRPVCVLIHPMSCFSIHKTRCAVAVCAVWVITSLAVVIMPFILITSTNTR 180
DB 121 ILFLTFISIRPVCVLIHPMSCFSIHKTRCAVAVCAVWVITSLAVVIMPFILITSTNTR 180

Db 121 ILFLTCFSIFRYCVIIHPMCSFSLHKTCAVAVCAVAVIISLVAVIPMTFLTISTNRTNR 180
Qy 181 SACLDTSSDELNTIKWNLILTAFTFCLPLVIVTLCYTTIIHTLHGLQDSCLOKAR 240
Db 181 SACLDTSSDELNTIKWNLILTAFTFCLPLVIVTLCYTTIIHTLHGLQDSCLOKAR 240
Qy 241 RLTLILLAFYVCELPFHILRVIRIESRLISCSISINOIHEAVIVSRPLAALMTFGNLL 300
Db 241 RLTLILLAFYVCELPFHILRVIRIESRLISCSISINOIHEAVIVSRPLAALMTFGNLL 300
Qy 301 LYVVSDNFOQAVCSIVRCVKVSGNLEQAKKISYSNNP 337
Db 301 LYVVSDNFOQAVCSIVRCVKVSGNLEQAKKISYSNNP 337

RESULT 2

US-10-270-144-2
Sequence 2, Application US/10270144
Publication No. US20030049790A1

GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui et al

TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

FILE REFERENCE: CLO00750CON

CURRENT APPLICATION NUMBER: US/10/270,144

CURRENT FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 60/205,196

PRIOR FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 337

TYPE: PRT

ORGANISM: Human

US-10-270-144-2

Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEPLDYLANASDFPDYAAAFGNCCTDENIPDKMHYLPVYIGIIFLVGPGNAVVISYIIF 60
Db 1 MNEPLDYLANASDFPDYAAAFGNCCTDENIPDKMHYLPVYIGIIFLVGPGNAVVISYIIF 60
Qy 61 KMRPKSSTIIMLACTDILYLSLPLHLYVASEGEMWIFGDMCKFIRSFHNLXSS 120
Db 61 KMRPKSSTIIMLACTDILYLSLPLHLYVASEGEMWIFGDMCKFIRSFHNLXSS 120
Qy 121 ILFLTCFSIFRYCVIIHPMCSFSLHKTCAVAVCAVAVIISLVAVIPMTFLTISTNRTNR 180
Db 121 ILFLTCFSIFRYCVIIHPMCSFSLHKTCAVAVCAVAVIISLVAVIPMTFLTISTNRTNR 180
Qy 181 SACLDTSSDELNTIKWNLILTAFTFCLPLVIVTLCYTTIIHTLHGLQDSCLOKAR 240
Db 181 SACLDTSSDELNTIKWNLILTAFTFCLPLVIVTLCYTTIIHTLHGLQDSCLOKAR 240
Qy 241 RLTLILLAFYVCELPFHILRVIRIESRLISCSISINOIHEAVIVSRPLAALMTFGNLL 300
Db 241 RLTLILLAFYVCELPFHILRVIRIESRLISCSISINOIHEAVIVSRPLAALMTFGNLL 300
Qy 301 LYVVSDNFOQAVCSIVRCVKVSGNLEQAKKISYSNNP 337
Db 301 LYVVSDNFOQAVCSIVRCVKVSGNLEQAKKISYSNNP 337

RESULT 3

US-10-188-405-8

Sequence 8, Application US/10188405

Publication No. US20030082585A1

GENERAL INFORMATION:

APPLICANT: Tian, Hui

APPLICANT: Dai, Kang

APPLICANT: Chen, Jin-Long
APPLICANT: Zhao, Jiaqiang
APPLICANT: Cutler, Gene
APPLICANT: Tularik Inc.
TITLE OF INVENTION: NO. US20030082585A1 Receptors
FILE REFERENCE: 018781-008410US
CURRENT APPLICATION NUMBER: US/10/188,405
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US 60/302,800
PRIOR FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 337
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: OTHER INFORMATION: human TGR164

US-10-188-405-8

Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEPLDYLANASDFPDYAAAFGNCCTDENIPDKMHYLPVYIGIIFLVGPGNAVVISYIIF 60
Db 1 MNEPLDYLANASDFPDYAAAFGNCCTDENIPDKMHYLPVYIGIIFLVGPGNAVVISYIIF 60
Qy 61 KMRPKSSTIIMLACTDILYLSLPLHLYVASEGEMWIFGDMCKFIRSFHNLXSS 120
Db 61 KMRPKSSTIIMLACTDILYLSLPLHLYVASEGEMWIFGDMCKFIRSFHNLXSS 120
Qy 121 ILFLTCFSIFRYCVIIHPMCSFSLHKTCAVAVCAVAVIISLVAVIPMTFLTISTNRTNR 180
Db 121 ILFLTCFSIFRYCVIIHPMCSFSLHKTCAVAVCAVAVIISLVAVIPMTFLTISTNRTNR 180
Qy 181 SACLDTSSDELNTIKWNLILTAFTFCLPLVIVTLCYTTIIHTLHGLQDSCLOKAR 240
Db 181 SACLDTSSDELNTIKWNLILTAFTFCLPLVIVTLCYTTIIHTLHGLQDSCLOKAR 240
Qy 241 RLTLILLAFYVCELPFHILRVIRIESRLISCSISINOIHEAVIVSRPLAALMTFGNLL 300
Db 241 RLTLILLAFYVCELPFHILRVIRIESRLISCSISINOIHEAVIVSRPLAALMTFGNLL 300
Qy 301 LYVVSDNFOQAVCSIVRCVKVSGNLEQAKKISYSNNP 337
Db 301 LYVVSDNFOQAVCSIVRCVKVSGNLEQAKKISYSNNP 337

RESULT 4

US-09-885-453-1

Sequence 1, Application US/09885453

Publication No. US20030088080A1

GENERAL INFORMATION:

APPLICANT: Communal, Didier

TITLE OF INVENTION: RECEPTOR GPCR10

FILE REFERENCE: 9409/2082

CURRENT APPLICATION NUMBER: US/09/885,453

PRIOR APPLICATION NUMBER: 2001-06-20

PRIOR FILING DATE: 2001-06-21

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 337

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: amino acid sequence GPCR10

LOCATION: (1)-(337)

OTHER INFORMATION: GPCR10 amino acid sequence

US-09-885-453-1

Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 KMRPKSSITIMLNACTDLTLTSLPFLIHYYASGENNIFGDMCKFRFSHFNLAYS 120
DB 61 KMRPKSSITIMLNACTDLTLTSLPFLIHYYASGENNIFGDMCKFRFSHFNLAYS 120
QY 121 IIFLCFSIFRCVLIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIPMFLITSTNRTR 180
DB 121 IIFLCFSIFRCVLIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIPMFLITSTNRTR 180
QY 181 SACLDITSSDELNTIKWMLILTATFCLPLVIVLCYTTIIHTLTHGLOTDSCLKOKAR 240
DB 181 SACLDITSSDELNTIKWMLILTATFCLPLVIVLCYTTIIHTLTHGLOTDSCLKOKAR 240
QY 241 RTIILLALAFYVCFPHILRVIRIESRLSISCSIEINOIHEAYIVSRPLALNTFGNLL 300
DB 241 RTIILLALAFYVCFPHILRVIRIESRLSISCSIEINOIHEAYIVSRPLALNTFGNLL 300
QY 301 LYVVVSDNFQOAVCSTVRCKVSGNLEQAKKISYSNNP 337
DB 301 LYVVVSDNFQOAVCSTVRCKVSGNLEQAKKISYSNNP 337

RESULT 5
US-09-943-798-4
; Sequence 4, Application US/09943798
; Patent No. US20020065215A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo Group Limited
; TITLE OF INVENTION: Polypeptide
; FILE REFERENCE: OG1021
; CURRENT APPLICATION NUMBER: US/09/943,798
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-943-798-4

Query Match 100.0%; Score 1771; DB 10; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNEPDIYLANASDPDYAAAFGNCNDENIPKMHYIPVYIGIIFLVGFGNAVISTYIF 60
QY 61 KMRPKSSITIMLNACTDLTLTSLPFLIHYYASGENNIFGDMCKFRFSHFNLAYS 120
DB 61 KMRPKSSITIMLNACTDLTLTSLPFLIHYYASGENNIFGDMCKFRFSHFNLAYS 120
QY 121 IIFLCFSIFRCVLIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIPMFLITSTNRTR 180
DB 121 IIFLCFSIFRCVLIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIPMFLITSTNRTR 180
QY 181 SACLDITSSDELNTIKWMLILTATFCLPLVIVLCYTTIIHTLTHGLOTDSCLKOKAR 240
DB 181 SACLDITSSDELNTIKWMLILTATFCLPLVIVLCYTTIIHTLTHGLOTDSCLKOKAR 240
QY 241 RTIILLALAFYVCFPHILRVIRIESRLSISCSIEINOIHEAYIVSRPLALNTFGNLL 300
DB 241 RTIILLALAFYVCFPHILRVIRIESRLSISCSIEINOIHEAYIVSRPLALNTFGNLL 300
QY 301 LYVVVSDNFQOAVCSTVRCKVSGNLEQAKKISYSNNP 337
DB 301 LYVVVSDNFQOAVCSTVRCKVSGNLEQAKKISYSNNP 337

DB 301 LYVVVSDNFQOAVCSTVRCKVSGNLEQAKKISYSNNP 337

RESULT 6
US-09-782-974C-86
; Sequence 86, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1e1 G Protein Coupled Receptor
; FILE REFERENCE: 41JUSPHM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-86

Query Match 90.5%; Score 1602.5; DB 9; Length 336;
Best Local Similarity 92.0%; Pred. No. 5.2e-137;
Matches 312; Conservative 6; Mismatches 14; Indels 7; Gaps 3;

QY 1 MNEPDIYLANASDPDYAAAFGNCNDENIPKMHYIPVYIGIIFLVGFGNAVISTYIF 60
DB 1 MNEPDIYLANASDPDYAAAFGNCNDENIPKMHYIPVYIGIIFLVGFGNAVISTYIF 60
QY 61 KMRPKSSITIMLNACTDLTLTSLPFLIHYYASGENNIFGDMCKFRFSHFNLAYS 120
DB 61 KMRPKSSITIMLNACTDLTLTSLPFLIHYYASGENNIFGDMCKFRFSHFNLAYS 120
QY 121 IIFLCFSIFRCVLIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIPMFLITSTNRTR 180
DB 121 IIFLCFSIFRCVLIHPMSCFSIHKTRCAVAVACAVWIIISLVAVIPMFLITSTNRTR 180
QY 181 SACLDITSSDELNTIKWMLILTATFCLPLVIVLCYTTIIHTLTHGLOTDSCLKOKAR 240
DB 181 SACLDITSSDELNTIKWMLILTATFCLPLVIVLCYTTIIHTLTHGLOTDSCLKOKAR 240
QY 241 RTIILLALAFYVCFPHILRVIRIESRLSISCSIEINOIHEAYIVSRPLALNTFGNLL 296
DB 241 RTIILLALAFYVCFPHILRVIRIESRLSISCSIEINOIHEAYIVSRPLALNTFGNLL 296
QY 297 GNLLYVVSDNFQOAVCSTVRCKVSGNLEQAKKISYSN 335
DB 297 GNLLYVVSDNFQOAVCSTVRCKVSGNLEQAKKISYSN 335

RESULT 7
US-09-943-798-2
Sequence 2, Application US/09943798
Patent No. US20020065215A1
GENERAL INFORMATION:
APPLICANT: Glaxo Group Limited
TITLE OF INVENTION: Polypeptide
FILE REFERENCE: OG1021
CURRENT APPLICATION NUMBER: US/09/943,798
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
US-09-943-798-2

Query Match 81.5%; Score 1444; DB 10; Length 276;
Best Local Similarity 100.0%; Pred. No. 8,7e-123;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 MRPKSTIIMLNACDLYLTLPLIHRYASGEWIRGDEPKRIRSFHNLVSSI 121
DB 1 MRPKSTIIMLNACDLYLTLPLIHRYASGEWIRGDEPKRIRSFHNLVSSI 60
QY 122 LFLFCGIFRCVLIHFMSCFSIKHTRCAVAVCAVWVNIISLVAVIPMTFLITSTNRNRS 181
DB 61 LFLFCGIFRCVLIHFMSCFSIKHTRCAVAVCAVWVNIISLVAVIPMTFLITSTNRNRS 120
QY 182 ACDDTSSDELNTIKWNLILFATFCLPLVIVLCTYTIHHTLHGLQDSCLOKARR 241
DB 121 ACDDTSSDELNTIKWNLILFATFCLPLVIVLCTYTIHHTLHGLQDSCLOKARR 180
QY 242 LFTLLAFVYCFPEHLIRIRIESRLSISCSIEQIHAVYSPRLALNFGNLL 301
DB 181 LFTLLAFVYCFPEHLIRIRIESRLSISCSIEQIHAVYSPRLALNFGNLL 240
QY 302 YVVVDNFQAVCSTVRCKVSGNLEQAKKISYNNP 337
DB 241 YVVVDNFQAVCSTVRCKVSGNLEQAKKISYNNP 276

RESULT 8
US-09-782-974C-60
Sequence 60, Application US/09782974C
Publication No. US20030082534A1
GENERAL INFORMATION:
APPLICANT: Vogel, Gabriel
APPLICANT: Lind, Peter
APPLICANT: Wood, Linda S.
APPLICANT: Parodi, Luis A.
TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
FILE REFERENCE: 41USPHER311
CURRENT APPLICATION NUMBER: US/09/782,974C
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/165,838
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 09/714,449
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 60/198,568
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/166,071
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,678
PRIOR FILING DATE: 1999-11-19
PRIOR APPLICATION NUMBER: 60/173,396
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/184,129
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 60/185,421
PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: 60/185,554
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/186,530
PRIOR FILING DATE: 2000-03-02
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 192
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-09-782-974C-60

Query Match 47.0%; Score 831.5; DB 9; Length 192;
Best Local Similarity 86.2%; Pred. No. 1.2e-67;
Matches 168; Conservative 6; Mismatches 14; Indels 7; Gaps 3;

QY 130 FRCVLIHFMSCFSIKHTRCAVAVCAVWVNIISLVAVIPMTFLITSTNRNRSACLDLTSS 189
DB 1 FRCVLIHFMSCFSIKHTRCAVAVCAVWVNIISLVAVIPMTFLITSTNRNRSACLDLTSS 60
QY 190 DELNTIKWNLILFATFCLPLVIVLCTYTIHHTLHGLQDSCLOKARRLITLLLA 249
DB 61 DELNTIKWNLILFATFCLPLVIVLCTYTIHHTLHGLQDSCLOKARRLITLLLA 120
QY 250 FYVCFPEHLIRVIRIESRLSISCSIEQIHAVYSPRLALNFGNLLVYV 305
DB 121 FYVCFPEHLIRVIRIESRLSISCSIEQIHAVYSPRLALNFGNLLVYV 177
QY 306 SDNFQAVCSTVRCK 320
DB 178 SDNFQAVCSTVRCK 192

RESULT 9
US-10-270-144-4
Sequence 4, Application US/10270144
Publication No. US20030049790A1
GENERAL INFORMATION:
APPLICANT: Wei, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
FILE REFERENCE: CL000750CON
CURRENT APPLICATION NUMBER: US/10/270,144
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/205,196
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 299
TYPE: PRT
ORGANISM: Mus musculus
US-10-270-144-4

Query Match 32.5%; Score 575; DB 9; Length 299;
Best Local Similarity 36.5%; Pred. No. 2.9e-44;
Matches 109; Conservative 67; Mismatches 119; Indels 4; Gaps 2;

QY 24 CTDENIPKMHVLPVYIGIIFLVGPGNAVISTYIFKMRPKSSTIIMLNACTDLYL 83
DB 1 CALKTGFOFYYPVAVYILVEIFIGLGNVAIMVFFHMRPKSGISVYMENLADFLYV 60
QY 84 TSLPELIHYASGNNWTFGDMCKLORFIHVNDGSLILFOTISAHRSYGAVYPLKSLG 120
DB 61 TSLPELIHYASGNNWTFGDMCKLORFIHVNDGSLILFOTISAHRSYGAVYPLKSLG 120
QY 144 IHRTRCAVAVCAVWVNIISLVAVIPMTFLITSTNRNRS-ACDDTSSDELNTIKWNLIL 202
DB 121 LKKNKAIYVSVLVVVAIVGPILEYSGTGRKKNKTVCYPTISNDYLRSEFISMCY 180
QY 203 TATFCLPLVIVLCTYTIHHTLHGLQDSCLOKARRLITLLAFVYCFPEHLIRV 262

Db 181 TVAMFCIPVLILGCGYLIVKALIVNDLNSPLRRKSIYLVIVLFAVVSYPFHVMT 240
 QY 263 IRESL---LSISCIENQIHEAVYISRPILALNFGNLLLVVSDNFQAVCSTVR 318
 Db 241 MNLRLDFOFPEMCDPNDRYATYQVTRGLASLNSCVPILYFLAGDFRRRLSRATR 299

RESULT 10

US-10-092-135-6

; Sequence 6, Application US/10092135
 ; Publication No. US20030054374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
 ; TITLE OF INVENTION: HGPBRMY27
 ; FILE REFERENCE: D0134.NP
 ; CURRENT APPLICATION NUMBER: US/10/092,135
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US 60/273,808
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/278,983
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 373
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-10-092-135-6

Query Match 32.0%; Score 567; DB 9; Length 373;
 Best Local Similarity 36.1%; Pred. No. 1,9e-43;
 Matches 108; Conservative 68; Mismatches 119; Indels 4; Gaps 2;

QY 24 CTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIFKMRPMKSTIIMLNACTDLVL 83
 Db 42 CALTKGFQFYLPVAVYLVIFLIGFNGSVAIMFVHMKPMGSIYVMEFNALADFLVY 101
 QY 84 TSLPFLHYHVSSENNIFGDFMCKFRFSFHFNLVYSILFLTFCISFRICVITIHPSCS 143
 Db 102 LTLPLILFYFNKTDIFGDMCKLRFIFHNLVYSILFLTFCISAHRSYGVYPLKSLG 161
 QY 144 IHKRCVAVACAVVWIIISLVAVIMPTFLITSTNTRNS-ACDLTSSDELNTIKWNLIL 202
 Db 162 RLKKAIAICISVWMLVVAISPIIFYSGTGVRKKKTTCTYTDSEIRLSIFYSMT 221
 QY 203 TATFGLPLVIVTLCTYTTIIFLTHGLQTDSCIKOKARLTIILLAFVYCLPFIILRV 262
 Db 222 TVAMFCVPLVILIGCYGLIVRALIYKDLNLSPLRRKSIYLVIVLFAVVSYPFHVMT 281
 QY 263 IRESL---LSISCIENQIHEAVYISRPILALNFGNLLLVVSDNFQAVCSTVR 318
 Db 282 MNLRLDFOFPEMCDPNDRYATYQVTRGLASLNSCVPILYFLAGDFRRRLSRATR 340

RESULT 11

US-10-092-135-3

; Sequence 3, Application US/10092135
 ; Publication No. US20030054374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
 ; TITLE OF INVENTION: HGPBRMY27
 ; FILE REFERENCE: D0134.NP
 ; CURRENT APPLICATION NUMBER: US/10/092,135
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US 60/273,808
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/278,983
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: GALLUS GALLUS
 US-10-092-135-3

Query Match 31.9%; Score 565.5; DB 9; Length 362;
 Best Local Similarity 35.0%; Pred. No. 2,6e-43;
 Matches 115; Conservative 66; Mismatches 137; Indels 11; Gaps 4;

QY 1 MNEPLDYLANASDFPYAA---AFGN---CTDENIPKMHYLPVYIGIIFLVGPGNAV 53
 Db 1 MTEALISAALNGTQPELLAGMAGNASTKCSLTKTGFOFYIIPYVILVIFIGFIGNSV 60
 QY 54 VISTYIFKMRPMKSTIIMLNACTDLVLTSLPFLIHYASGEMNIFGDFMCKFRFS 113
 Db 61 AIMFVFNHMPMGISIVMNLALFVLVLPALIFEFNKTDMIFGDMCKLDRFIF 120
 QY 114 HFNLYSILFLTFCISFRICVITIHPSCSIHKRCVAVACAVVWIIISLVAVIMPTFLI- 172
 Db 121 HFNLYSILFLTFCISVHRTGVVHPLKSLGRLLKKNVAVVSSLVMAVVAIVAPILFYS 180
 QY 173 TSTNTRNSACDLTSSDELNTIKWNLILFATFGLPLVIVTLCTYTTIIFLTHGLQTD 232
 Db 181 TGVRRMKTTCTYTDSEIRLSYFVSMCTYVMEFIPVILIGCYGLIVKALIVRDLDN 240
 QY 233 SCLKOKARLTIILLAFVYCLPFIILRVIRRESL---LSISCIENQIHEAVYISRP 289
 Db 241 SPLRRKSIYLVIVLFAVVSYPFHVMTLNRLRLDFOFPEMCDPNDRYATYQVTRG 300
 QY 290 IALNFGNLLLVVSDNFQAVCSTVR 318
 Db 301 LASLNSCVPILYFLAGDFRRRLSRATR 329

RESULT 12

US-10-092-135-4

; Sequence 4, Application US/10092135
 ; Publication No. US20030054374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
 ; TITLE OF INVENTION: HGPBRMY27
 ; FILE REFERENCE: D0134.NP
 ; CURRENT APPLICATION NUMBER: US/10/092,135
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US 60/273,808
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/278,983
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: MELEAGRIS GALLOPAVO
 US-10-092-135-4

Query Match 31.9%; Score 565.5; DB 9; Length 362;
 Best Local Similarity 35.0%; Pred. No. 2,6e-43;
 Matches 115; Conservative 66; Mismatches 137; Indels 11; Gaps 4;

QY 1 MNEPLDYLANASDFPYAA---AFGN---CTDENIPKMHYLPVYIGIIFLVGPGNAV 53
 Db 1 MTEALISAALNGTQPELLAGMAGNASTKCSLTKTGFOFYIIPYVILVIFIGFIGNSV 60
 QY 54 VISTYIFKMRPMKSTIIMLNACTDLVLTSLPFLIHYASGEMNIFGDFMCKFRFS 113
 Db 61 AIMFVFNHMPMGISIVMNLALFVLVLPALIFEFNKTDMIFGDMCKLDRFIF 120
 QY 114 HFNLYSILFLTFCISFRICVITIHPSCSIHKRCVAVACAVVWIIISLVAVIMPTFLI- 172
 Db 121 HFNLYSILFLTFCISVHRTGVVHPLKSLGRLLKKNVAVVSSLVMAVVAIVAPILFYS 180

RESULT 15
US-10-092-135-5
; Sequence 5, Application US/10092135
; Publication No. US20030054374A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company

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Db      121  GGCAATATCTCTGCTGGGATTTCCAGCAATCAGTAGTATATCCATTACATTTTC 180
Qy      181  AAATAGAGACCTTGGAGAGCAGCACCATCATATATGCGACTGGCCCTGCAGATCTG 240
Db      181  AAATAGAGACCTTGGAGAGCAGCACCATCATATATGCGACTGGCCCTGCAGATCTG 240
Qy      241  CTGTATCTGACACCTCCCTCCCTGATTCAGTACTATGCGAGTGGGAAACCTGATC 300
Db      241  CTGTATCTGACACCTCCCTCCCTGATTCAGTACTATGCGAGTGGGAAACCTGATC 300
Qy      301  TTGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Db      301  TTGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Qy      361  ATCCCTTCCCTCAGCTGTTTCAGCATCTCCGCTACTGATGATGATGATGATGATGATG 420
Db      361  ATCCCTTCCCTCAGCTGTTTCAGCATCTCCGCTACTGATGATGATGATGATGATGATG 420
Qy      421  TGCCTTTCCATTCACAAACTCGATGTCAGCTTGTAGCTGTGCTGTGCTGTGATTCAT 480
Db      421  TGCCTTTCCATTCACAAACTCGATGTCAGCTTGTAGCTGTGCTGTGCTGTGATTCAT 480
Qy      481  TCAGTGTAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db      481  TCAGTGTAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Qy      541  TCAGCTGTCTCGACTCAGCATGTCAGTGTGATGATGATGATGATGATGATGATGATG 600
Db      541  TCAGCTGTCTCGACTCAGCATGTCAGTGTGATGATGATGATGATGATGATGATGATG 600
Qy      601  ATTTGACTGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db      601  ATTTGACTGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy      661  ATATACACACTGTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Db      661  ATATACACACTGTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Qy      721  AGGCTAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db      721  AGGCTAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy      781  AGGCTCATTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db      781  AGGCTCATTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Qy      841  CATAAGCTTACATGCTTTCTAGACCATTTAGCTGCTGCTGACACCTTTGGTAACTGTTA 900
Db      841  CATAAGCTTACATGCTTTCTAGACCATTTAGCTGCTGCTGACACCTTTGGTAACTGTTA 900
Qy      901  CTATATGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
Db      901  CTATATGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
Qy      961  GTAAAGCGGGAACCTTGAGCAAGCAAAAGAAATTTAGTTAACTCAAAACCCCTTGA 1014
Db      961  GTAAAGCGGGAACCTTGAGCAAGCAAAAGAAATTTAGTTAACTCAAAACCCCTTGA 1014

```

RESULT 2

US-10-270-144-1

; Sequence 1, Application US/10270144

; Publication No. US20030049790A1

; GENERAL INFORMATION:

; APPLICANT: WEI, Ming-Hui et al

; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

; FILE REFERENCE: CLO00750CON

; CURRENT APPLICATION NUMBER: US/10/270,144

; CURRENT FILING DATE: 2002-10-15

; PRIOR APPLICATION NUMBER: 60/205,196

; PRIOR FILING DATE: 2000-05-18

```

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Human
US-10-270-144-1
Query Match      99.8%; Score 1012.4; DB 9; Length 1014;
Best Local Similarity 99.9%; Pred. No. 8e-301;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ATGATGAGCCAGTACGATATTTAGCAAAATGCTTGTATTTCCCGATTTATGACGCTG 60
Db      1  ATGATGAGCCAGTACGATATTTAGCAAAATGCTTGTATTTCCCGATTTATGACGCTG 60
Qy      61  TTTGGAATTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
Db      61  TTTGGAATTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
Qy      61  TTTGGAATTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
Db      61  TTTGGAATTTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
Qy      121  GGCAATATCTCTGCTGGGATTTCCAGCAATCAGTAGTATATCCATTACATTTTC 180
Db      121  GGCAATATCTCTGCTGGGATTTCCAGCAATCAGTAGTATATCCATTACATTTTC 180
Qy      181  AAATAGAGACCTTGGAGAGCAGCACCATCATATATGCGACTGGCCCTGCAGATCTG 240
Db      181  AAATAGAGACCTTGGAGAGCAGCACCATCATATATGCGACTGGCCCTGCAGATCTG 240
Qy      241  CTGTATCTGACACCTCCCTCCCTGATTCAGTACTATGCGAGTGGGAAACCTGATC 300
Db      241  CTGTATCTGACACCTCCCTCCCTGATTCAGTACTATGCGAGTGGGAAACCTGATC 300
Qy      301  TTGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Db      301  TTGAGATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Qy      361  ATCCCTTCCCTCAGCTGTTTCAGCATCTCCGCTACTGATGATGATGATGATGATGATG 420
Db      361  ATCCCTTCCCTCAGCTGTTTCAGCATCTCCGCTACTGATGATGATGATGATGATGATG 420
Qy      421  TGCCTTTCCATTCACAAACTCGATGTCAGCTTGTAGCTGTGCTGTGCTGTGATTCAT 480
Db      421  TGCCTTTCCATTCACAAACTCGATGTCAGCTTGTAGCTGTGCTGTGCTGTGATTCAT 480
Qy      481  TCAGTGTAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db      481  TCAGTGTAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Qy      541  TCAGCTGTCTCGACTCAGCATGTCAGTGTGATGATGATGATGATGATGATGATGATG 600
Db      541  TCAGCTGTCTCGACTCAGCATGTCAGTGTGATGATGATGATGATGATGATGATGATG 600
Qy      601  ATTTGACTGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db      601  ATTTGACTGCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy      661  ATATACACACTGTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Db      661  ATATACACACTGTGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
Qy      721  AGGCTAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db      721  AGGCTAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy      781  AGGCTCATTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db      781  AGGCTCATTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Qy      841  CATAAGCTTACATGCTTTCTAGACCATTTAGCTGCTGCTGACACCTTTGGTAACTGTTA 900
Db      841  CATAAGCTTACATGCTTTCTAGACCATTTAGCTGCTGCTGACACCTTTGGTAACTGTTA 900
Qy      901  CTATATGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960

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Qy	1	ATGAAATGAGCAGCTAGACACTATTACCAAAATGCTTGTATTTTCCCGGATATGACAGCTGCT	60
Db	1	ATGAATGAGCCACTGACACTATTTTAGCAAAATGCTTGTATTTTCCCGGATATGACAGCTGCT	60
Qy	61	TTTGGAAATGCACTGATGATAAAACATGCCACTCAAGATGCACTACCTCCCTGTTATTAT	120
Db	61	TTTGGAAATGCACTGATGATAAAACATGCCACTCAAGATGCACTACCTCCCTGTTATTAT	120
Qy	121	GGCATTATCTTCCCTGCGGGATTTTCAGGCAATGCAGTAGTATATCCACTTACATTTTC	180
Db	121	GGCATTATCTTCCCTGCGGGATTTTCAGGCAATGCAGTAGTATATCCACTTACATTTTC	180
Qy	181	AAAATAGACCTTGGAAAGCAGCAACATCATTTATGTGAACCGGGCTGCACAGACTG	240
Db	181	AAAATAGACCTTGGAAAGCAGCAACATCATTTATGTGAACCGGGCTGCACAGACTG	240
Qy	241	CTGTATCTACACAGCCTCCCTTCCCTGATTACTACTTGGCAGTGGCGAAACTGGATC	300
Db	241	CTGTATCTACACAGCCTCCCTTCCCTGATTACTACTTGGCAGTGGCGAAACTGGATC	300
Qy	301	TTTGGAGATTCAATGTAAGTTTATTCGCGTTACAGCTTCATTTCAACTGTATAGAGC	360
Db	301	TTTGGAGATTCAATGTAAGTTTATTCGCGTTACAGCTTCATTTCAACTGTATAGAGC	360
Qy	361	ATCCCTTCCCTACCGTTTGAGCATCTTCGCGTACGTGTGATCATTTCAACCAATAGC	420
Db	361	ATCCCTTCCCTACCGTTTGAGCATCTTCGCGTACGTGTGATCATTTCAACCAATAGC	420
Qy	421	TGCTTTCCATTACAAAACCTGAGTGCAGTTGTAGCCTGCTGTGTGGATCATTT	480
Db	421	TGCTTTCCATTACAAAACCTGAGTGCAGTTGTAGCCTGCTGTGTGGATCATTT	480
Qy	481	TCACGTGTAGCTGTCAATTCGATGACTTTTGTATCAGATCAACCAACGAGACCACAGA	540

[illegible]

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Db      121 GGCATTATCTCTCGTGGGATTTCCAGGCAATGCACTAGTATATCCACTTACATTTTC 180
QY      181 AAATGAGACCTTGAAGAGACAGCACCATCATTTATGCTGAAGCTGGCCCTGACAGATCTG 240
Db      181 AAATGAGACCTTGAAGAGACAGCACCATCATTTATGCTGAAGCTGGCCCTGACAGATCTG 240
QY      241 CTGTATCTGACAGCCTCCCTTCCTGATTCAGTACTAGTCCAGTGGCGAAAACCTGATC 300
Db      241 CTGTATCTGACAGCCTCCCTTCCTGATTCAGTACTAGTCCAGTGGCGAAAACCTGATC 300
QY      301 TTGGAGATTTCATGTAAGTATATCCGCTTACAGCTTCATTTCAACCTGATATAGAGC 360
Db      301 TTGGAGATTTCATGTAAGTATATCCGCTTACAGCTTCATTTCAACCTGATATAGAGC 360
QY      361 ATCCCTTCTCCTCAGCTGTTCACAGCATCTCCGCTACTGTGTATCATTTACCAACATGAGC 420
Db      361 ATCCCTTCTCCTCAGCTGTTCACAGCATCTCCGCTACTGTGTATCATTTACCAACATGAGC 420
QY      421 TCGTTTCCATTACAAAACCTGCATGCGATGCGATGCGTGTGCTGTGTGTGATCAT 480
Db      421 TCGTTTCCATTACAAAACCTGCATGCGATGCGATGCGTGTGCTGTGTGTGATCAT 480
QY      481 TCACGTGATGCTGTTCAGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATG 540
Db      481 TCACGTGATGCTGTTCAGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATG 540
QY      541 TCAGCCTGTCTGACCTCAGCAGCTGCGATGCGATGCGATGCGATGCGATGCGATGCGATG 600
Db      541 TCAGCCTGTCTGACCTCAGCAGCTGCGATGCGATGCGATGCGATGCGATGCGATGCGATG 600
QY      601 ATTTTACGTGCACTACTTCTGCTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db      601 ATTTTACGTGCACTACTTCTGCTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY      661 ATATACCACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 720
Db      661 ATATACCACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 720
QY      721 AGGCTATACCTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 780
Db      721 AGGCTATACCTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 780
QY      781 AGGCTATACCTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 840
Db      781 AGGCTATACCTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 840
QY      841 CATGAAGCTTACATCTGTTCTAGACCATTTAGCTGCTGTGACACCTTTGGTAACCTGTTA 900
Db      841 CATGAAGCTTACATCTGTTCTAGACCATTTAGCTGCTGTGACACCTTTGGTAACCTGTTA 900
QY      901 CTATATGCTGTGCTGACGCAAACTTTCAGCAGCTGTCTGCTCAACAGTGAATGCAAA 960
Db      901 CTATATGCTGTGCTGACGCAAACTTTCAGCAGCTGTCTGCTCAACAGTGAATGCAAA 960
QY      961 GTTAAGGGGGAACCTTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1014
Db      961 GTTAAGGGGGAACCTTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1014

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RESULT 5
US-09-943-798-3
; Sequence 3, Application US/09943798
; Patent No. US20020065215A1
; GENERAL INFORMATION:
; APPLICANT: Glaxo Group Limited
; TITLE OF INVENTION: Polypeptide
; FILE REFERENCE: 061021
; CURRENT APPLICATION NUMBER: US/09/943, 798
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1014

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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-943-798-3
Query Match      99.88; Score 1012.4; DB 10; Length 1014;
Best Local Similarity 99.98; Pred. No. 8e-301;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ATGATAGGACCTAGACATTTAGCAAAATGCTTCTGATTTCCCGATATGACAGCTGCT 60
Db      1 ATGATAGGACCTAGACATTTAGCAAAATGCTTCTGATTTCCCGATATGACAGCTGCT 60
QY      61 TTGGAAATTTGCACTGATGAAACATCCACTCAAGATGCACTACCTCCCTGATTTAT 120
Db      61 TTGGAAATTTGCACTGATGAAACATCCACTCAAGATGCACTACCTCCCTGATTTAT 120
QY      121 GGCATTATCTCTCGTGGGATTTCCAGGCAATGCACTAGTATATCCACTTACATTTTC 180
Db      121 GGCATTATCTCTCGTGGGATTTCCAGGCAATGCACTAGTATATCCACTTACATTTTC 180
QY      181 AAATGAGACCTTGAAGAGACAGCACCATCATTTATGCTGAAGCTGGCCCTGACAGATCTG 240
Db      181 AAATGAGACCTTGAAGAGACAGCACCATCATTTATGCTGAAGCTGGCCCTGACAGATCTG 240
QY      241 CTGTATCTGACAGCCTCCCTTCCTGATTCAGTACTAGTCCAGTGGCGAAAACCTGATC 300
Db      241 CTGTATCTGACAGCCTCCCTTCCTGATTCAGTACTAGTCCAGTGGCGAAAACCTGATC 300
QY      301 TTGGAGATTTCATGTAAGTATATCCGCTTACAGCTTCATTTCAACCTGATATAGAGC 360
Db      301 TTGGAGATTTCATGTAAGTATATCCGCTTACAGCTTCATTTCAACCTGATATAGAGC 360
QY      361 ATCCCTTCTCCTCAGCTGTTCACAGCATCTCCGCTACTGTGTATCATTTACCAACATGAGC 420
Db      361 ATCCCTTCTCCTCAGCTGTTCACAGCATCTCCGCTACTGTGTATCATTTACCAACATGAGC 420
QY      421 TCGTTTCCATTACAAAACCTGCATGCGATGCGATGCGTGTGCTGTGTGATCAT 480
Db      421 TCGTTTCCATTACAAAACCTGCATGCGATGCGATGCGTGTGCTGTGTGATCAT 480
QY      481 TCACGTGATGCTGTTCAGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATG 540
Db      481 TCACGTGATGCTGTTCAGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATG 540
QY      541 TCAGCCTGTCTGACCTCAGCAGCTGCGATGCGATGCGATGCGATGCGATGCGATGCGATG 600
Db      541 TCAGCCTGTCTGACCTCAGCAGCTGCGATGCGATGCGATGCGATGCGATGCGATGCGATG 600
QY      601 ATTTTACGTGCACTACTTCTGCTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db      601 ATTTTACGTGCACTACTTCTGCTCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY      661 ATATACCACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 720
Db      661 ATATACCACTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 720
QY      721 AGGCTATACCTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 780
Db      721 AGGCTATACCTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 780
QY      781 AGGCTATACCTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 840
Db      781 AGGCTATACCTGTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 840
QY      841 CATGAAGCTTACATCTGTTCTAGACCATTTAGCTGCTGTGACACCTTTGGTAACCTGTTA 900
Db      841 CATGAAGCTTACATCTGTTCTAGACCATTTAGCTGCTGTGACACCTTTGGTAACCTGTTA 900
QY      901 CTATATGCTGTGCTGACGCAAACTTTCAGCAGCTGTCTGCTCAACAGTGAATGCAAA 960
Db      901 CTATATGCTGTGCTGACGCAAACTTTCAGCAGCTGTCTGCTCAACAGTGAATGCAAA 960
QY      961 GTTAAGGGGGAACCTTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1014

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Db 961 GTAAGCGGACCTTGAGCAGCAAGAAATTAAGTACTCAACACCTTGA 1014

RESULT 6

US-10-270-144-3

Sequence 3, Application US/10270144

Publication No. US20030049790A1

GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui et al

TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

FILE REFERENCE: C1000750CON

CURRENT APPLICATION NUMBER: US/10/270,144

PRIOR FILING DATE: 2002-10-15

PRIOR APPLICATION NUMBER: 60/205,196

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 9905

TYPE: DNA

ORGANISM: Human

US-10-270-144-3

Query Match

Best Local Similarity 99.8%; Score 1012.4; DB 9; Length 9905;

Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 961 GTAAGCGGACCTTGAGCAGCAAGAAATTAAGTACTCAACACCTTGA 1014

1 ATGAATGAGCCACTAGACTATTATAGCAATGCTTCGTGATTTCCCGATTTATGAGCTGCT 60

8309 ATGAATGAGCCACTAGACTATTATAGCAATGCTTCGTGATTTCCCGATTTATGAGCTGCT 8368

61 TTGGAAATGACACTGATGAAACATCCCACTCAAGAGCAGTACTGCTGCTTATAT 120

8369 TTGGAAATGACACTGATGAAACATCCCACTCAAGAGCAGTACTGCTGCTTATAT 8428

121 GGCATTATCTCTGCTGAGGATTTCCAGGCAATGAGTATGATATCCACTATGATTTTC 180

8429 GGCATTATCTCTGCTGAGGATTTCCAGGCAATGAGTATGATATCCACTATGATTTTC 8488

181 AAAATGAGACCTTGGAGAGCAGCAGCAGCAGTATGATGCTGAGCTGCTGAGATCTG 240

8489 AAAATGAGACCTTGGAGAGCAGCAGCAGCAGTATGATGCTGAGCTGCTGAGATCTG 8548

241 CTGATCTGACCAAGCTCCCTCTCTGATCTACTATGATGATGAGGAGGAGGAGGATG 300

8549 CTGATCTGACCAAGCTCCCTCTCTGATCTACTATGATGATGAGGAGGAGGAGGATG 8608

301 TTGGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360

8609 TTGGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 8668

361 ATCT 420

8669 ATCT 8728

421 TCCCTTTCCATTCACAAAACCTGAGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 480

8729 TCCCTTTCCATTCACAAAACCTGAGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 8788

481 TCAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 540

8789 TCAGTGTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 8848

541 TCAGCTGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 600

8849 TCAGCTGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 8908

601 ATTTGACTGCAACTACTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660

8909 ATTTGACTGCAACTACTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8968

QY 661 ATTATCCACACTCTGACCCATGAGTCAAACTGACAGCTGACCTTAAGCAAGAAAGCAGCA 720

8969 ATTATCCACACTCTGACCCATGAGTCAAACTGACAGCTGACCTTAAGCAAGAAAGCAGCA 9028

QY 721 AGGCTAACCATTTCTGCTACTCTCTGATTTTACATGATGATTTTACCCTTCATATCTTG 780

9029 AGGCTAACCATTTCTGCTACTCTCTGATTTTACATGATGATTTTACCCTTCATATCTTG 9088

QY 781 AGGCTATTCGATGCAATCTGCTGCTCTTCAATCATGATGATTTTCAATGATGATGATG 840

9089 AGGCTATTCGATGCAATCTGCTGCTCTTCAATCATGATGATTTTCAATGATGATGATG 9148

QY 841 CATTGAGCTTACATGCTTCTGACCATTAAGCTGCTGCAACCTTGGTAACTGCTTA 900

9149 CATTGAGCTTACATGCTTCTGACCATTAAGCTGCTGCTGCAACCTTGGTAACTGCTTA 9208

QY 901 CTATATGCTGTGCTGAGCAGCAACTTTCAGAGGCTGTCTGCTCAACAGTGAAGTCAAA 960

9209 CTATATGCTGTGCTGAGCAGCAACTTTCAGAGGCTGTCTGCTCAACAGTGAAGTCAAA 9268

QY 961 GTAAGCGGACCTTGAGCAGCAAGAAATTAAGTACTCAACACCTTGA 1014

9269 GTAAGCGGACCTTGAGCAGCAAGAAATTAAGTACTCAACACCTTGA 9322

Db 961 GTAAGCGGACCTTGAGCAGCAAGAAATTAAGTACTCAACACCTTGA 1014

RESULT 7

US-09-782-974C-85

Sequence 85, Application US/09782974C

Publication No. US20030082534A1

GENERAL INFORMATION:

APPLICANT: Vogell, Gabriel

APPLICANT: Lind, Peter

APPLICANT: Wood, Linda S.

TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor

FILE REFERENCE: 41USPHM311

CURRENT APPLICATION NUMBER: US/09/782,974C

PRIOR FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: 60/165,838

PRIOR FILING DATE: 1999-11-16

PRIOR APPLICATION NUMBER: 09/714,449

PRIOR FILING DATE: 2000-11-16

PRIOR APPLICATION NUMBER: 60/198,568

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: 60/166,071

PRIOR FILING DATE: 1999-11-17

PRIOR APPLICATION NUMBER: 60/166,678

PRIOR FILING DATE: 1999-11-19

PRIOR APPLICATION NUMBER: 60/173,396

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: 60/184,129

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: 60/185,421

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: 60/185,554

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: 60/186,530

PRIOR FILING DATE: 2000-03-02

Remaining Prior Application data removed - See file wrapper or PALM.

NUMBER OF SEQ ID NOS: 192

SOFTWARE: PatentIn version 3.1

SEQ ID NO 85

LENGTH: 1020

TYPE: DNA

ORGANISM: Homo sapiens

US-09-782-974C-85

Query Match

Best Local Similarity 96.3%; Score 976.2; DB 9; Length 1020;

Matches 1011; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 1 ATGAATGAGCCACTAGACTATTATAGCAATGCTTCGTGATTTCCCGATTTATGAGCTGCT 60

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Db      4 ATGAATGAGCCACTAGCTATTGAGCAAAATGCTTGATTTCCCGGATATGAGCGTCT 63
QY      61 TTGGAAATTCGACTGATGAAAACATCCACTCAAGATGACTACCCCTGTTATTTAT 120
Db      64 TTGGAAATTCGACTGATGAAAACATCCACTCAAGATGACTACCCCTGTTATTTAT 123
QY      121 GGCATTATCTCTCTCGTGGGATTTCCAGGCAATGACAGTAGTATATCCATTATTTTC 180
Db      124 GGCATTATCTCTCTCGTGGGATTTCCAGGCAATGACAGTAGTATATCCATTATTTTC 183
QY      181 AAAATGAGACCTTGGAGAGACAGCAGCATATATGATGAACTGGCGCTCAGAGATCTG 240
Db      184 AAAATGAGACCTTGGAGAGACAGCAGCATATATGATGAACTGGCGCTCAGAGATCTG 243
QY      241 CTGTATCTGACACGCTCCCTCTCTGATTCAGTACTATGATCCAGTGGCGAAAATGATC 300
Db      244 CTGTATCTGACACGCTCCCTCTCTGATTCAGTACTATGATCCAGTGGCGAAAATGATC 303
QY      301 TTGGAGATTTCAATGTTGTAAGTTTATCCGCTTCAGCTTCATTCAACCTGTATAGCAGC 360
Db      304 TTGGAGATTTCAATGTTGTAAGTTTATCCGCTTCAGCTTCATTCAACCTGTATAGCAGC 363
QY      361 ATCCCTTCTCCTACCTGTTTCAGACATCTTCCGCTACTGTGTGATCATTTCAACCAATGAGC 420
Db      364 ATCCCTTCTCCTACCTGTTTCAGACATCTTCCGCTACTGTGTGATCATTTCAACCAATGAGC 423
QY      421 TGCCTTTCCATTACAAAACCTCGATGTCAGTTGTCAGCTGTGCTGTGGTGGATCATTT 480
Db      424 TGCCTTTCCATTACAAAACCTCGATGTCAGTTGTCAGCTGTGCTGTGGTGGATCATTT 483
QY      481 TCACGTGTAAGCTGTATCCGATGACCTTCTTGATCATCAATCAACCAAGAGCAACAGA 540
Db      484 TCACGTGTAAGCTGTATCCGATGACCTTCTTGATCATCAATCAACCAAGAGCAACAGA 543
QY      541 TCAGCTGTCTGACCTCAGCAATTTGGGATGAATCAATATCTATTAAGTGTGTACAACTTA 600
Db      544 TCAGCTGTCTGACCTCAGCAATTTGGGATGAATCAATATCTATTAAGTGTGTACAACTTA 603
QY      601 AATTTGACTGCAACTACTTTCTGCTTCCCTTGGTGTATGATGACACTTTGCTATACACG 660
Db      604 AATTTGACTGCAACTACTTTCTGCTTCCCTTGGTGTATGATGACACTTTGCTATACACG 663
QY      661 AATTTGACTGCAACTACTTTCTGCTTCCCTTGGTGTATGATGACACTTTGCTATACACG 720
Db      664 AATTTGACTGCAACTACTTTCTGCTTCCCTTGGTGTATGATGACACTTTGCTATACACG 723
QY      721 AGGCTAACCATCTGCTACTCTTGCATTTTACGATGTTTATACCTTCCATATCTTG 780
Db      724 AGGCTAACCATCTGCTACTCTTGCATTTTACGATGTTTATACCTTCCATATCTTG 783
QY      781 AGGCTAACCTC-GGATGCAATCTC-GCCTGCTTTCATATGATGTTGCTCATTTGAGAAATCAGA 838
Db      784 AGGCTAACCTCAGATGCAATCTCAGCTGCTTTCATATGATGTTGCTCATTTGAGAAATCAGA 843
QY      839 TCCATTAAGCTTACATCTGTTTCTAGACATTA-GCTGCTCTGAACACCTTTGTTAACTTG 897
Db      844 TCCATTAAGCTTACATCTGTTTCTAGACATTA-GCTGCTCTGAACACCTTTGTTAACTTG 903
QY      898 TTACTATATGTGTGTGTCAGCGCACTTTCAGCAGGCTGTGCTGCTCAACAGAGATGTC 957
Db      904 TTACTATATGTGTGTGTCAGCGCACTTTCAGCAGGCTGTGCTGCTCAACAGAGATGTC 963
QY      958 AAAGTAAAGCGGAGACCTTGAGCAAGCAAGAAATTAAGTTACTCAACAACCTTTGA 1014
Db      964 AAAGTAAAGCGGAGACCTTGAGCAAGCAAGAAATTAAGTTACTCAACAACCTTTGA 1020

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RESULT 8
 US-09-943-798-1
 ; Sequence 1, Application US/09943798
 ; Patent No. US20020065215A1
 ; GENERAL INFORMATION:

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; APPLICANT: Glaxo Group Limited
; TITLE OF INVENTION: Polypeptide
; FILE REFERENCE: OG1021
; CURRENT APPLICATION NUMBER: US/09/943,798
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ. ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ. ID NO 1
; LENGTH: 831
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-943-798-1

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Query Match      81.8%; Score 829.4; DB 10; Length 831;
Best Local Similarity 99.9%; Pred. No. 1.4e-244;
Matches 830; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      184 ATGAGACCTTGGAGAGACAGCAGCATATATGCTGAACCTGGCGCTGACAGATCTGCTG 243
Db      1 ATGAGACCTTGGAGAGACAGCAGCATATATGCTGAACCTGGCGCTGACAGATCTGCTG 60
QY      244 TATCTGACAGCCTCCCTCTCTGATTCAGTACTATGACGAGCGGCAAACTGATCTTT 303
Db      61 TATCTGACAGCCTCCCTCTCTGATTCAGTACTATGACGAGCGGCAAACTGATCTTT 120
QY      304 GGAGATTTCAATGTTGTAAGTTTATCCGCTTCAGCTTCATTCAACCTGTATAGCAGATC 363
Db      121 GGAGATTTCAATGTTGTAAGTTTATCCGCTTCAGCTTCATTCAACCTGTATAGCAGATC 180
QY      364 CTCTTCTCCTACCTGTTTCAGACATCTTCCGCTACTGTGTATCATTTCAACCAATGAGCTGC 423
Db      181 CTCTTCTCCTACCTGTTTCAGACATCTTCCGCTACTGTGTATCATTTCAACCAATGAGCTGC 240
QY      424 TTTTTCATTACAAAACCTCGATGTCAGTTGTCAGCTGTGCTGTGGTGGATCATTTTCA 483
Db      241 TTTTTCATTACAAAACCTCGATGTCAGTTGTCAGCTGTGCTGTGGTGGATCATTTTCA 300
QY      484 CTGTGAGCTGTATCCGATGACCTTCTTGATCATCAACCAAGAGCAACAGATCA 543
Db      301 CTGTGAGCTGTATCCGATGACCTTCTTGATCATCAACCAAGAGCAACAGATCA 360
QY      544 GCTGTCTGACCTCAGCACTTTGGGATGAATCAATATCTATTAAGTGTGTACAACTTAAT 603
Db      361 GCTGTCTGACCTCAGCACTTTGGGATGAATCAATATCTATTAAGTGTGTACAACTTAAT 420
QY      604 TTGACGCAACTACTTTCTGCTTCCCTTGGTGTATGATGACACTTTGCTATACAGATT 663
Db      421 TTGACGCAACTACTTTCTGCTTCCCTTGGTGTATGATGACACTTTGCTATACAGATT 480
QY      664 ATCCACACTCTGACCAATGAGCTGCAAACTGACAGCTGCTTAAAGCAAGAGCAGAGAG 723
Db      481 ATCCACACTCTGACCAATGAGCTGCAAACTGACAGCTGCTTAAAGCAAGAGCAGAGAG 540
QY      724 CTACCATCTCTGCTACTCTTGCATTTTACGATGTTTATACCTTCCATATCTTGAG 783
Db      541 CTACCATCTCTGCTACTCTTGCATTTTACGATGTTTATACCTTCCATATCTTGAG 600
QY      784 GTCAATTCGAGTCAATCTGCGCTGTTTCAATAGTGTTCATTTGAGATGAGATCATCAT 843
Db      601 GTCAATTCGAGTCAATCTGCGCTGTTTCAATAGTGTTCATTTGAGATGAGATCATCAT 660
QY      844 GAAGCTTAACATCTGTTCTAGACATTAAGCTGCTCTGAACACCTTTGTTAACTGTTACTA 903
Db      661 GAAGCTTAACATCTGTTCTAGACATTAAGCTGCTCTGAACACCTTTGTTAACTGTTACTA 720
QY      904 TATGTGTGTGTGTCAGCGCACTTTCAGCAGGCTGTGCTGCTCAACAGAGATGTC 963
Db      721 TATGTGTGTGTGTCAGCGCACTTTCAGCAGGCTGTGCTGCTCAACAGAGATGTC 780
QY      964 AGCGGAGACCTTGAGCAAGCAAGAAATTAAGTTACTCAACAACCTTTGA 1014
Db      781 AGCGGAGACCTTGAGCAAGCAAGAAATTAAGTTACTCAACAACCTTTGA 831

```


RESULT 9

US-09-728-422-1

Sequence 1, Application US/09728422

Patent No. US20020128187A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Zhou, Ping

APPLICANT: Goodrich, Ryle

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Ren, Feiyan

APPLICANT: Zhao, Qing A.

APPLICANT: Yang, Yonghong

APPLICANT: Wehrman, Tom

APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. US20020128187A1el Nucleic Acids and

FILE REFERENCE: Polypeptides

CURRENT APPLICATION NUMBER: US/09/728,422

CURRENT FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: 09/560,875

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR FILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 10

SOFTWARE: pt_FL_genes Version 2.0

SEQ ID NO 1

LENGTH: 1313

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (547)..(1239)

US-09-728-422-1

Query Match

Best Local Similarity 99.7%; Score 728; DB 10; Length 1313;

Matches 740; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 ATGATGAGGCACTAGACATTTTATGCAATGCTTCTGATTTCCCGCATTTATGACGCTCT 60
DB 547 ATGATGAGGCACTAGACATTTTATGCAATGCTTCTGATTTCCCGCATTTATGACGCTCT 606
QY 61 TTGGAAATGGCACTAGTAAATCCCAATGCAATGACATGACATGCTCCCTGATTTAT 120
DB 607 TTGGAAATGGCACTAGTAAATCCCAATGCAATGACATGACATGCTCCCTGATTTAT 666
QY 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGACATGATGATATCCACTTACATTTTC 180
DB 667 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGACATGATGATATCCACTTACATTTTC 726
QY 181 AAATAGACCTTGGAGAGACACACCATCATTTATCTGAACTGCGCTGCACAGATCTG 240
DB 727 AAATAGACCTTGGAGAGACACACCATCATTTATCTGAACTGCGCTGCACAGATCTG 786
QY 241 CTGTATCTGACGACCTCCCTCCCTGATGATGATGATGATGATGATGATGATGATGATG 300
DB 787 CTGTATCTGACGACCTCCCTCCCTGATGATGATGATGATGATGATGATGATGATGATG 846
QY 301 TTGGAGATTTTCACTGTAAGTTTATCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 360
DB 847 TTGGAGATTTTCACTGTAAGTTTATCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT 906
QY 361 ATCCCTTCTCTCACTGTTTACAGATCTTCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 420
DB 907 ATCCCTTCTCTCACTGTTTACAGATCTTCCGCTTCCAGCTTCCAGCTTCCAGCTTCCAG 966
QY 421 TGGTTTCACTTACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 967 TGGTTTCACTTACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026
QY 481 TCACTGGTACGTCTCATTCGATGATGATGATGATGATGATGATGATGATGATGATGATG 540

RESULT 10

US-09-782-974C-59/C

Sequence 59, Application US/09782974C

Publication No. US20030082534A1

GENERAL INFORMATION:

APPLICANT: Vogeli, Gabriel

APPLICANT: Lind, Peter

APPLICANT: Wood, Linda S.

APPLICANT: Parodi, Luis A.

TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor

FILE REFERENCE: 411USPHM311

CURRENT APPLICATION NUMBER: US/09/782,974C

CURRENT FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: 60/165,838

PRIOR FILING DATE: 1999-11-16

PRIOR APPLICATION NUMBER: 60/144,449

PRIOR FILING DATE: 1999-11-17

PRIOR APPLICATION NUMBER: 60/166,678

PRIOR FILING DATE: 1999-11-19

PRIOR APPLICATION NUMBER: 60/173,396

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: 60/184,129

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: 60/185,421

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: 60/185,554

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: 60/186,530

PRIOR FILING DATE: 2000-03-02

Remainder of prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 192

SOFTWARE: PatentIn version 3.1

SEQ ID NO 59

LENGTH: 578

TYPE: DNA

ORGANISM: Homo sapiens

US-09-782-974C-59

Query Match

Best Local Similarity 53.0%; Score 537.2; DB 9; Length 578;

Matches 572; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 387 CTTCGGTACTGTGTGATCATTCACCAATGAGCTGCTTTCATTCACAAACTGAGT 446
DB 578 CTTCGGTACTGTGTGATCATTCACCAATGAGCTGCTTTCATTCACAAACTGAGT 519
QY 447 TGCAGTTGAGCCTGTGCTGT 506
DB 518 TGCAGTTGAGCCTGTGCTGT 459

[illegible]

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Db      60 CTTGGAGAAATGGTTGGCAACAGAGGCTATCTGAATAGTACTACCTCTCGCAATTT 119
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      119 ATGGCAATTAATCTTCTCGTGGGATTTCCAGGCAAGCAAGTAGTAATCCATTACATTT 178
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      120 ATGCATTCAGATTCATATTTTGGAGCTCTGGGAAATGTCACTGTGGTTCGGCTACCTCT 179
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      179 TCAAAATGAGACCTTGGGAAGGAGGACACATCTATTATGCGAATCGGGCTGACAGATC 238
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      180 TGTGCATGGAAGAACTGGAAAGGAGGAAATGTCTATCTTTTAACTCTTTCATCTTGACT 239
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      239 TCGTGTATGTGACCAAGCCTCCCTCTCTGATTCATCACTATGCGAGTGGGAAATCGA 238
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      240 TTGCTTTCTGTGGACACCTTCCATCTGTATTAAGATTATGGCAAT -- GATTAAGGGA 236
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      299 TCTTTGGACATTTCAATGTGTAACTTTATCCGCTTCAAGCTTCCATTTCAACCTGTATAGA 358
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      297 CCTATGGAAATGTCTCTGTATATAGAACACCGAATATGTCTTACACCAACCTCTACCA 356
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      359 GCATCTCTTCCGACCTGTTTACAGATCTCCGTAAGTGTGATGATTCATCCACCAATGA 418
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      357 GCATCTCTTCTCTCACTTTTCATTTAGATGAGACCGAATATCTGTCAATGAAATACCTTTCC 416
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      419 GCTGCTTTTCCATTCACAAATCTGATGTGCAATGTAGCCGTGCTGTGGTGTGATCA 478
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      417 GAGAACACTTTCTACAAAAGAAAGAAATTTGCCATTTTAATCTGGCTGTCTGGGCT 476
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      479 TTTCACTGTAGCTGTCAATTCGAGTACCTTTCTTGATCACAATCAACCAAGAACACA 538
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      477 TAGTGACCTTAGAAGTTCTAACCCATCTCACTTTCATCAATTTGTCGCCAAAAGAGG 536
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      539 GATCAGCCGTCTCCAGACCTCACCAAGTTGG ----- ATGAACCTAATCAATTAAGGT 592
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      537 GGATGACGTGCACTAGCACTATGCAAGTTGTGGAACCCGTGAACCAATCTCATTTTACAGC 596
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      593 ACAACCTAATTTTGTGACCTGCAACTATTTTCTGCTCCCTGGTGATAGTACACTTTGCT 652
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      597 TCTGCTGACTTTGTGGGCTTCTCTAATTCCTCTCTCTGTGATGTGCTTTCTACTACA 656
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      653 ATACACGATTAATCCACACTGTGACCCATGAGATGAGCAAACTGACAGCTGCTTAAGCA 712
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      657 AGATGTAGTCTCTTAAGAGAGAGGAGGACGACGAGAAGCAACTGCCCTCCACTGGACA 716
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      713 AAGCAGGAAGGCTAACCAATTCCTCTACTCTCTTGATATGATGTTTAACTCTCC 772
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      717 AACCCCAAGCGCTGTGTGGCTGGCGGTTGTGTATCTCTATACCTTCCACACCTATC 776
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      773 ATATCTTGAAGGTCATTTGGATGGAGATTCGAGCTG 807
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      777 ATATCATGGCAATTTGAGAGATGCCCTCACGCGTG 811
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-077-173A-1
: Sequence 1, Application US/09077173A
: Publication No. US20030082674A1
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: RECEPTOR AND NUCLEIC ACID MOLECULE ENCODING
: NUMBER OF SEQUENCES: 4
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/077,173A
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/BE 96/00123
: FILING DATE:
: INFORMATION FOR SEQ ID NO: 1:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 13:43:23 ; Search time 27 Seconds
(without alignments)
367.242 Million cell updates/sec

Title: US-10-023-775b-2

Perfect score: 1771

Sequence: 1 MNEPDIYLANSDFPDYAA.....RCVSGNLEQAKKISYNNP 337

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Maximum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	564.5	31.9	362	3	US-08-513-974B-374 Sequence 374, App
2	562	31.7	373	2	US-08-559-524A-4 Sequence 4, App11
3	562	31.7	373	3	US-08-749-707-4 Sequence 4, App11
4	477	26.9	373	3	US-08-513-974B-373 Sequence 373, App
5	467	26.4	334	2	US-08-559-524A-2 Sequence 2, App11
6	467	26.4	334	3	US-08-749-707-2 Sequence 2, App11
7	438	24.7	375	1	US-08-442-134A-2 Sequence 2, App11
8	438	24.7	375	1	US-08-444-581B-2 Sequence 2, App11
9	438	24.7	375	1	US-08-446-088A-2 Sequence 2, App11
10	438	24.7	375	2	US-08-559-524A-3 Sequence 3, App11
11	438	24.7	375	3	US-08-749-707-3 Sequence 3, App11
12	421	23.8	328	3	US-08-513-974B-39 Sequence 39, App1
13	421	23.8	328	3	US-08-513-974B-371 Sequence 371, App
14	406.5	23.0	327	3	US-08-513-974B-372 Sequence 372, App
15	404	22.8	357	5	PCT-US95-07180-3 Sequence 3, App11
16	400	22.6	328	3	US-08-513-974B-56 Sequence 56, App1
17	400	22.6	328	3	US-08-513-974B-360 Sequence 380, App
18	397	22.4	357	4	US-09-266-464-2 Sequence 4, App11
19	394.5	22.3	339	1	US-08-153-848-44 Sequence 44, App1
20	394.5	22.3	339	2	US-08-812-871-3 Sequence 3, App11
21	394.5	22.3	339	3	US-09-299-843A-44 Sequence 44, App1
22	394.5	22.3	339	4	US-09-088-337B-44 Sequence 44, App1
23	394.5	22.3	339	5	PCT-US93-11153-44 Sequence 44, App1
24	394.5	22.3	339	5	PCT-US95-07180-2 Sequence 2, App11
25	391.5	22.1	395	1	US-08-097-938-5 Sequence 5, App11
26	391.5	22.1	395	1	US-08-476-000-5 Sequence 5, App11
27	391.5	22.1	395	1	US-08-472-840-5 Sequence 5, App11

28	391.5	22.1	395	2	US-08-476-976-5 Sequence 5, App11
29	391.5	22.1	395	3	US-08-474-410-5 Sequence 5, App11
30	388.5	21.9	328	3	US-08-459-046-2 Sequence 2, App11
31	388.5	21.9	395	4	US-08-486-673B-2 Sequence 2, App11
32	388.5	21.9	395	4	US-08-486-673B-5 Sequence 5, App11
33	388.5	21.9	399	1	US-08-476-000-61 Sequence 61, App1
34	388.5	21.9	399	1	US-08-472-840-61 Sequence 61, App1
35	388.5	21.9	399	2	US-08-476-976-61 Sequence 61, App1
36	388.5	21.9	399	3	US-08-474-410-61 Sequence 61, App1
37	388.5	21.9	399	4	US-08-486-673B-61 Sequence 61, App1
38	388.5	21.9	425	1	US-07-657-769B-69 Sequence 69, App1
39	388.5	21.9	425	1	US-08-097-938-7 Sequence 7, App11
40	388.5	21.9	425	1	US-08-313-553-13 Sequence 13, App1
41	388.5	21.9	425	1	US-07-789-184-220 Sequence 220, App
42	388.5	21.9	425	1	US-08-476-000-7 Sequence 7, App11
43	388.5	21.9	425	1	US-08-475-263-220 Sequence 220, App
44	388.5	21.9	425	1	US-08-472-840-7 Sequence 7, App11
45	388.5	21.9	425	1	US-08-485-886-220 Sequence 220, App

ALIGNMENTS

RESULT 1
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohnaka, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhito
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357

FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-513-974B-374

Query Match 31.9%; Score 564.5; DB 3; Length 362;
Best Local Similarity 35.0%; Pred. No. 9.1e-37;

Matches 115; Conservative 66; Mismatches 135; Indels 11; Gaps 4;

QY 1 MNEPLDVLAVASDPDYAA--AFGN---CTDENIPDKMHYLPVIGIIFLVGFPGNAV 53
DB 1 MTEALISALANGPPELLAGMAGNATTKCSLTKGFQYIPLPVYIIVFIFGLNSV 60
QY 54 VISTYFKMRPMKSTTLMNLACTDLVLTSLPELIHYVASEGNMIFGDMCKFIRESF 113
DB 61 AIMFEFMRPMGSIYVMENLALDELVLTLPALIFYYFNKTDWIFGDMCKLQRFIF 120
QY 114 HENLYSILFLGCFSTFRVCVITTHPMSCFTHKTRCAVAVCAVMIISLVAVIPMTLIT 173
DB 121 HNVLSILFLGCFSTFRVCVITTHPMSCFTHKTRCAVAVCAVMIISLVAVIPMTLIT 180
QY 174 STNRTRS-ACDLTSSDELNTIKWNLITATTCPLVIVLCYTTIHTLTHGLQTD 232
DB 181 IGRNRKTKTCYPTFADEVLRSEYVSMCTVMEFCIPYIIGCYLIKALIKRLDN 240
QY 233 SCUKAKARLTILLALFAVYCFPLHLIRVIRIESRL--LSISCSLENGIHEAYIVSRP 289
DB 241 SPLRRKSTYIVITLVFAVSYLPLFHVMTLNLRLRDLFQTPQMCANDRVYATYQVTRG 300
Y 290 LALNTEGNLLTVVVSNDNOQAVCSIVR 318
DB 301 LASLNSCVDPILYFLAGDIFRRRLSRATR 329

RESULT 2

US-08-559-524A-4
Sequence 4, Application US/08559524A
Patent No. 5871963
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
City: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-00-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-559-524A-4

Query Match 31.7%; Score 562; DB 2; Length 373;
Best Local Similarity 36.1%; Pred. No. 1.5e-36;

Matches 108; Conservative 67; Mismatches 120; Indels 4; Gaps 2;

QY 24 CTDENIPDKMHYLPVIGIIFLVGFPGNAVISTYIFKMRPMKSTTLMNLACTDLVLT 83
DB 42 CALTKGFQYIPLPVYIIVFIFGLNSVAIMFEFMRPMGSIYVMENLALDELVLT 101
QY 84 TSLPELIHYVASEGNMIFGDMCKFIRESFHPNLVYSILFLGCFSTFRVCVITTHPMSCFS 143
DB 102 LTLPALIFYFNKTDWIFGDMCKLQRFIFHVDYGLFLPTCISAHRSYGVYPLKSLG 161
QY 144 IHTRCVAVCAVMIISLVAVIPMTLITSTNRTRS-ACDLTSSDELNTIKWNLIT 202
DB 162 RLKKNVAVISLVAVIPMTLITSTNRTRS-ACDLTSSDELNTIKWNLIT 221
QY 203 TATTCPLVIVLCYTTIHTLTHGLQTDSCUKAKARLTILLALFAVYCFPLHLIRV 262
DB 222 TVAMFCVPLVILIGCYLIKALIKRLDNLSPLRRKSTYIVITLVFAVSYLPLFHVMT 281
QY 263 IRIESRL--LSISCSLENGIHEAYIVSRPLALNTEGNLLTVVVSNDNOQAVCSIVR 318
DB 282 MNLRLRDLFQTPQMCANDRVYATYQVTRGLASLNSCVDPILYFLAGDIFRRRLSRATR 340

RESULT 3

US-08-749-707-4
Sequence 4, Application US/08749707
Patent No. 6063582
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:


```

; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5596088th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,134A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sidley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-442-134A-2

Query Match      24.7%; Score 438; DB 1; Length 375;
Best Local Similarity 33.0%; Pred. No. 6.3e-27;
Matches 93; Conservative 59; Mismatches 118; Indels 12; Gaps 4;

QY 28 NIPLMKHYLPVYIGIIFLVGFGNNAVISTYIFKMRPKSSTIMLNACTDLYLTSLP 87
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 28 NEDFYVLLPVSYGVCVGLCLNMGVLYIFLCRLKTNASTTMEHFLAVSDALYAASLP 87
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 88 FLIHYYASGEMNIFGDMCKRTFSFHFNLVSSILFLGCSIFRCVVIITHMPCSIHKT 147
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 88 LLVYYIYARGDHMFSTVLCIKVRFLEYTLVLCISILFLTCISVHRCIGVLRPLRSRMGHA 147
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 148 RCVAACAVWMIISLVAVIPMTFLTSTNRTNRSCDLTSSDELTNTIKWMLILATTF 207
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 148 RYARRVAGAVWVLVLAQAPVLYEVTTSAR--GPLTCHDSAPLELSRFVAYSSVMGLGF 206
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 208 CLPLVIVLCYTTIHTL-----THGIQDSCCLKOKARRLTILLLAFYVCFPLPHIL 260
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 207 AVPEFVILVLCYLMARRLRLKPAVGTSGGLPR---AKRSKVRITIAVLAVLAFALCFPEHVT 263
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 261 RVIRIESRLISTSCSIENQIHEAVYISRPALANFGNLLY 302
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 264 RLTYYSFRSLDLSCHTLNAINMAYKTR-LASANSCLDPEVLY 304
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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RESULT 8
US-08-444-581B-2
; Sequence 2, Application US/08444581B
; Patent No. 5607836
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.

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; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5607836th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,581B
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/442,134
; FILING DATE: 16-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sidley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-581B-2

Query Match      24.7%; Score 438; DB 1; Length 375;
Best Local Similarity 33.0%; Pred. No. 6.3e-27;
Matches 93; Conservative 59; Mismatches 118; Indels 12; Gaps 4;

QY 28 NIPLMKHYLPVYIGIIFLVGFGNNAVISTYIFKMRPKSSTIMLNACTDLYLTSLP 87
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 28 NEDFYVLLPVSYGVCVGLCLNMGVLYIFLCRLKTNASTTMEHFLAVSDALYAASLP 87
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    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 88 FLIHYYASGEMNIFGDMCKRTFSFHFNLVSSILFLGCSIFRCVVIITHMPCSIHKT 147
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    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 88 LLVYYIYARGDHMFSTVLCIKVRFLEYTLVLCISILFLTCISVHRCIGVLRPLRSRMGHA 147
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 148 RCVAACAVWMIISLVAVIPMTFLTSTNRTNRSCDLTSSDELTNTIKWMLILATTF 207
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 148 RYARRVAGAVWVLVLAQAPVLYEVTTSAR--GPLTCHDSAPLELSRFVAYSSVMGLGF 206
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 208 CLPLVIVLCYTTIHTL-----THGIQDSCCLKOKARRLTILLLAFYVCFPLPHIL 260
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DB 207 AVPEFVILVLCYLMARRLRLKPAVGTSGGLPR---AKRSKVRITIAVLAVLAFALCFPEHVT 263
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    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 261 RVIRIESRLISTSCSIENQIHEAVYISRPALANFGNLLY 302
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 264 RLTYYSFRSLDLSCHTLNAINMAYKTR-LASANSCLDPEVLY 304
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
US-08-446-088A-2
; Sequence 2, Application US/08446088A
; Patent No. 5691156
; GENERAL INFORMATION:

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Query Match	24.7%;	Score 438;	DB 2;	Length 375;
Best Local Similarity	33.0%;	Pred. No. 6.3e-27;		
Matches	93;	Conservative	59;	Mismatches 118;
			Indels	12;
			Gaps	4

[illegible]

RESULT 11
US-08-749-707-3
Sequence 3, Application US/08749707
Patent No. 6063582
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington

RESULT 12
US-08-513-974B-39
Sequence 39, Application US/08513974B
Patent No. 611439
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohbi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA

```

: ZIP: 02109
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/513,974B
: FILING DATE: 14-SEP-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/JP95/01599
: FILING DATE: 10-AUG-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-093989
: FILING DATE: 19-AUG-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-057186
: FILING DATE: 16-MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 7-007177
: FILING DATE: 20-JAN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-326611
: FILING DATE: 28-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-270017
: FILING DATE: 02-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-236357
: FILING DATE: 30-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-236356
: FILING DATE: 30-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189274
: FILING DATE: 11-AUG-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189273
: FILING DATE: 11-AUG-1945
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 6-189272
: FILING DATE: 11-AUG-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Resnick, David S.
: REGISTRATION NUMBER: 34,235
: REFERENCE/DOCKET NUMBER: 45753
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-523-3400
: TELEFAX: 617-523-6440
: INFORMATION FOR SEQ ID NO: 39:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 328 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
:
: US-08-513-974B-39
:
: Query Match 23.8%; Score 421; DB 3; Length 328;
: Best Local Similarity 32.9%; Pred. No. 1,2e-25;
: Matches 96; Conservative 45; Mismatches 125; Indels 26; Gaps 5;
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: Oy 36 LPVYIGILFLVGFPGNAVISTYIFKKRPWKSSPTIIMANLACTDLYLTSIPPLHYTAS 95
: Db 29 LTPYISVAVLVGLPLNCVIAQAICASRRTLTIRSAVYTYTILALADLMTACSPDLLLYNAR 88
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: Oy 96 GENMVFEDDMCKFRFSFHFNLYSILFLTCFSIFRYCVIIHPMSCFEIHK---TRCAVY 152
: Db 89 GDHHPFDLACRFYRFLFYANLHGSILFLTCISFORVYIGICHPLA--SMHNRGGRAMV 146
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: Oy 153 ACAVWVITSLVAVIPMTFLITSTNRKNSACLDTSSDELTFTKYNILITATTCPLVY 212

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Db 147 VCGVWLVATVTAOCPLPAVFAATGIQRNRVTCYDLSPIILSTRVLPYGMALTVIGFLPFI 206
QY 213 IVTLCTYTTIHTLTHGLQTDSC-----LKOKARRLTLLLAIFYVCFLLPHIL 260
Db 207 ALLACVORMARRL-----CRQDGPAGVADGRSKARMAVVAAYVAISFLPHIT 258
QY 261 RVIRIESRL-SISCSIENQIHEAYIVSRPLAALNTFGNLLVYVSDNFQO 311
Db 259 KTAIVLAVRSTPGVSCPVLETFMAAYKGTREFAVSNSVLDPLIFYFTQOKFR 310

RESULT 13
US-08-513-974B-371
; Sequence 371, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhito
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272

FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-6440
TELEFAX: 617-523-3400
INFORMATION FOR SEQ ID NO: 371:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-513-974B-371

Query Match 23.8%; Score 421; DB 3; Length 328;
Best Local Similarity 32.9%; Pred. No. 1.2e-25;
Matches 96; Conservative 45; Mismatches 125; Indels 26; Gaps 5;

QY 36 LPVYIGIIFVGPNAVVISYIFKMRPMSSTIILNLAAGTDLVLTSLPLIHYAS 95
Db 29 LTFYTSVVLVVGPLNLCVIAQICASRRITLRSVYTLNLALDLMACSLPLIYAR 88
QY 96 GEMWIFGDMCKTFRSEFHNLYSSILFLCFSTFRYCVIITHMCSFSIHK---TRCAV 152
Db 89 GDHMFEDLACRFVRFLEFVNLHGSILFLCISFRYLGICHPLA--SWHKGGRRAWY 146
QY 153 ACAVWIIISLVAVIPMFELTSTNRTRSACDLTSSDELNTKWNLLITATFCPLV 212
Db 147 VCGVWLVATVTAOCPLPAVFAATGIQRNRVTCYDLSPIILSTRVLPYGMALTVIGFLPFI 206
QY 213 IVTLCTYTTIHTLTHGLQTDSC-----LKOKARRLTLLLAIFYVCFLLPHIL 260
Db 207 ALLACVORMARRL-----CRQDGPAGVADGRSKARMAVVAAYVAISFLPHIT 258
QY 261 RVIRIESRL-SISCSIENQIHEAYIVSRPLAALNTFGNLLVYVSDNFQO 311
Db 259 KTAIVLAVRSTPGVSCPVLETFMAAYKGTREFAVSNSVLDPLIFYFTQOKFR 310

RESULT 14
US-08-513-974B-372
; Sequence 372, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhito
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599

FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017
 FILING DATE: 02-NOV-1994
 PRIOR APPLICATION DATA:
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 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 372:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 327 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-513-974B-372

Query Match 23.0%; Score 406.5; DB 3; Length 327;
 Best Local Similarity 33.8%; Pred. No. 1.5e-24;
 Matches 96; Conservative 46; Mismatches 131; Indels 11; Gaps 6;

QY 36 LPVYIGITFLVGFPGNAVISTYIFKMRPMKSSITIMLNLACTDLILYTSPLFIHYA 95
 DB 29 LTPVSVYLVVGLPNICVIAQICASRRITLRSAYVTIMLADLMTACSLPLLYNVAR 88
 QY 96 GENMIFGDMCKFRFSEFHNLSILFLTCFSIFRYCVIHPMCSFSIHK--TRCAVY 152
 DB 89 CDHMFPGDLACRFVFLRYANLHGSILFLTCISFORYIGICHPLA--SHKKGRRAMV 146
 QY 153 ACAVWT-LSLVAVIPMTFLITSTNRNSACLDLTSDELNTIKMYNLILATFTCLPL 211
 DB 147 VGVVWVLAATACLTAAFAATGIOR-NRTVCYDLSPLITSTRVLPYGMALVIGPLPE 205
 QY 212 VAVITCYTTIITLTHGQTDSCLKQ---KARLITLILLALAYVCFPLHILVIRIESR 268
 DB 206 IALLACYCMARRLCRDGPAGVPAQERSKARMAVAAVAISFLPEHITKTAYLAVR 265
 QY 269 IL-SISCSIEQNIHEAVYISRLALNTFGNLLVYVSDNQ 311
 DB 266 STPGVSCVLETFFAAYKGTGTFASVNLDPILTFYTOOKRR 309

RESULT 15

PCT-US95-07180-3
 Sequence 3, Application PC/TUS9507180
 GENERAL INFORMATION:
 APPLICANT: LI, YI
 APPLICANT: GOCAYNE, JEANINE D
 APPLICANT: RUBEN, STEVEN M
 TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBER69
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ADDRESSEE: STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NJ
 COUNTRY: US
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/07180
 FILING DATE: 06-JUNE-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: MULLINS, J.G.
 REGISTRATION NUMBER: 30,073
 REFERENCE/DOCKET NUMBER: 325800-366
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1744
 TELEFAX: 201-994-1700
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 357 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-07180-3

Query Match 22.8%; Score 404; DB 5; Length 357;
 Best Local Similarity 30.3%; Pred. No. 2.6e-24;
 Matches 89; Conservative 72; Mismatches 125; Indels 8; Gaps 5;

QY 35 YLPVYIGITFLVGFPGNAVISTYIFKMRPMKSSITIMLNLACTDLILYTSPLFIHYA 94
 DB 42 FMPVYTYIFIVLSPLNVLAIYFVLRMKVKKPAAVYMDLMAVDLFFVSLPSKISYFE 101
 QY 95 GENMIFGDMCKFRFSEFHNLSILFLTCFSIFRYCVIHPMCSFSIHKTRCAVAC 154
 DB 102 SGTDMFGSGMCRFATAAYINMYASIMLATVYISIDRLAVYPIQSLSWRLGAGNFTC 161
 QY 155 AVWTISLVAVIPMTFLITSTNRT--NRSACLDLTSDELNTI-KWYNLILATFTCLP 210
 DB 162 VIVWVWALMGVPL-LKRGQTRVPLNTTCHDLSLMLMGFSYVSARSALFEFLVP 220
 QY 211 LVAVITCYTTIITLTHGQTDSCLKQKARRITLILLALFYVCFPLHILVIRIESRL 270
 DB 221 LIVSTVCYSIIRCLSSSAVANRSKSRALFLSAVFCIFVCFGTNLLLVHY--LFL 278
 QY 271 SISCSIEQNIHEAVYISRLALNTFGNLLVYVSDNQAVGSTRCKVSGN 324
 DB 279 SDSPGTE-AAFYALICVYTSVSCIDPLIYYASSECRLHYSILCKESSD 331

Search completed: May 30, 2003, 13:47:54
 Job time : 28 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 29, 2003, 21:37:48 ; Search time 2792 Seconds

(without alignments)
10569.572 Million cell updates/sec

Title: US-10-023-775B-1

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1014	100.0	1014	6	AX305130	AX305130 Sequence
2	1014	100.0	1014	6	AX464561	AX464561 Sequence
3	1012.4	99.8	1014	6	AX148186	AX148186 Sequence
4	1012.4	99.8	1014	6	AX379468	AX379468 Sequence
5	1012.4	99.8	1014	6	AX384211	AX384211 Sequence
6	1012.4	99.8	1014	6	AB083598	AB083598 Homo sapi
7	1012.4	99.8	1014	9	AF411109	AF411109 Homo sapi
8	1012.4	99.8	1081	6	AX458238	AX458238 Sequence
9	1012.4	99.8	1092	9	AF370886	AF370886 Homo sapi
10	1012.4	99.8	1414	9	AB065877	AB065877 Homo sapi
11	1012.4	99.8	9905	6	AX379470	AX379470 Sequence
12	1012.4	99.8	67645	9	AL356486	AL356486 Human DNA
13	1012.4	99.8	156555	9	AC026756	AC026756 Homo sapi
14	1010.8	99.7	1729	6	AX191332	AX191332 Sequence
15	976.2	96.3	1020	6	AX147840	AX147840 Sequence
16	735.6	72.5	202838	2	AC108794	AC108794 Mus muscu
17	537.2	53.0	578	6	AX147814	AX147814 Sequence
18	332	32.7	2245	6	AX384210	AX384210 Sequence
19	189	18.6	657	6	AX244775	AX244775 Sequence
20	161.2	15.9	1977	5	AF031897	AF031897 Metagris
21	158.6	15.6	1293	10	MM022829	U22829 Mus muscu
22	158.6	15.6	3204	10	MM022830	U22830 Rattus norv
23	153.8	15.2	12630	10	MM024536	AJ245636 Mus muscu
24	153.8	15.2	288763	2	AC124692	AC124692 Mus muscu
25	148.6	14.7	1312	9	S81950	S81950 P2 purinoc
26	148.6	14.7	1426	9	HS042029	U42029 Human P2Y1
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28	148.6	14.7	16178	9	HS04569	AJ006945 Human P2Y
29	148.6	14.7	176170	2	AC021662	AC021662 Homo sapi
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31	147.6	14.6	73949	2	AC105795	AC105795 Rattus no
32	147	14.5	1308	4	BT034041	U34041 Bos taurus
33	147	14.5	1666	4	BT0298CP	X87628 B.taurus mr
34	144.2	14.2	2231	5	AF242850	AF242850 Raja erin
35	143	14.1	2951	5	AF432354	AF432354 Xenopus l
36	134.8	13.3	1163	5	GDP2Y3	X98283 G.domesticu
37	134.2	13.2	136930	5	AL590151	AL590151 Zebrafish
38	133.2	13.1	1074	5	AF069555	AF069555 Metagris
39	132.6	13.1	3055	11	HSATPRMR	Z49205 H.sapiens m
40	130.8	12.9	2361	5	XL2P2Y8	G28604 human STS S
41	130.8	12.9	91107	2	AC116265	AC116265 Rattus no
42	129.8	12.8	192524	2	AC120742	AC120742 Rattus no
43	129.8	12.8	209273	2	AC121579	AC121579 Mus muscu
44	129.6	12.8	1325	9	AF247785	AF247785 Homo sapi
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ALIGNMENTS

RESULT 1	AX305130	1014 bp	DNA	linear	PAT 11-DEC-2001
LOCUS	AX305130	Sequence 10 from Patent WO0187937.			
DEFINITION	AX305130				
ACCESSION	AX305130.1	GI:17644765			
VERSION					
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens.				
REFERENCE					
AUTHORS	Patterson,C., Lu,D.A., Thornton,M., Lu,Y., Tribouley,C.M., Grau,R., Khan,F.A., Gandhi,A.R., Walla,N.K., Nguyen,D.B., Yue,H., Hafalla,A., Elliott,V.S., Lal,P., Reddy,R., Kallick,D.A., Tang,T.Y.				

and Au-Young, J.
G-protein coupled receptors
Patent: WO 0187937-A 10-22-NOV-2001;
Incyte Genomics, Inc. (US)

FEATURES
source
1. 1014
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 6575963CB1"
BASE COUNT 259 a 263 c 188 g 304 t
ORIGIN

Query Match 100.0%; Score 1014; DB 6; Length 1014;
Best Local Similarity 100.0%; Pred. No. 8.7e-258;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAGCCACAGACTATTATGCAAAATGCTTGATTTCCCGATATGACAGCTCT 60
DB 1 ATGATGAGCCACAGACTATTATGCAAAATGCTTGATTTCCCGATATGACAGCTCT 60

QY 61 TTGGAATTTGCACTGATGAAACATCCCACTCAAGATGACATCTCCCTGTTATTTAT 120
DB 61 TTGGAATTTGCACTGATGAAACATCCCACTCAAGATGACATCTCCCTGTTATTTAT 120

QY 121 GGCATTATCTCTCGTGGGATTTCCAGGCAATGCACTAGTATTCACCTTACATTTTC 180
DB 121 GGCATTATCTCTCGTGGGATTTCCAGGCAATGCACTAGTATTCACCTTACATTTTC 180

QY 181 AATATGAGCCTTGGAGAGACGACATCATTTATGCGAACCGGCTGCACAGATCTG 240
DB 181 AATATGAGCCTTGGAGAGACGACATCATTTATGCGAACCGGCTGCACAGATCTG 240

QY 241 CTGATCTGACACAGCTCCCTTCCTGATTCATCTACTATGCGAGTGGGAAACCTGATC 300
DB 241 CTGATCTGACACAGCTCCCTTCCTGATTCATCTACTATGCGAGTGGGAAACCTGATC 300

QY 301 TTGGAATTTGCACTGATGAAACATCCCACTCAAGATGACATCTCCCTGTTATTTAT 360
DB 301 TTGGAATTTGCACTGATGAAACATCCCACTCAAGATGACATCTCCCTGTTATTTAT 360

QY 361 ATCCCTCTCCACCTGTTTCAGATCTCCGCTGCTGATGATGATGATGATGATGATG 420
DB 361 ATCCCTCTCCACCTGTTTCAGATCTCCGCTGCTGATGATGATGATGATGATGATG 420

QY 421 TGCCTTTCCATTCACAAACCTGATGATGATGATGATGATGATGATGATGATGATG 480
DB 421 TGCCTTTCCATTCACAAACCTGATGATGATGATGATGATGATGATGATGATGATG 480

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DB 481 TCATGCTAGCTGATTCGAGATCTCTGATGATGATGATGATGATGATGATGATGATG 540

QY 541 TCAGCCGTCTGACCTCACCAGTTCGATGATGATGATGATGATGATGATGATGATG 600
DB 541 TCAGCCGTCTGACCTCACCAGTTCGATGATGATGATGATGATGATGATGATGATG 600

QY 601 ATTTGAGTCACTGATCTCTGCTCCCTGCTGATGATGATGATGATGATGATGATG 660
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QY 661 ATTATTCACACTGACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 720
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QY 721 AGGCTAACATCTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
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QY 781 AGGCTAACATCTGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
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QY 841 CATGAGCTTACATGTTCTTACAGCATGATGCTGCTGACACACCTTGTACCTGTTA 900

DB 841 CATGAGCTTACATGTTCTTACAGCATGATGCTGCTGACACACCTTGTACCTGTTA 900
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QY 961 GTAGCGGGAACCTTGGAGCAAGCAAAATATGTTACTGCAACCAACCTTTGA 1014
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RESULT 2
AX464561 1014 bp DNA linear PAT 16-JUL-2002
LOCUS AX464561
DEFINITION Sequence 1 from Patent EP1219638.
ACCESSION AX464561
VERSION AX464561.1 GI:21899357
KEYWORDS

ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Fildock, M.D.
G-protein coupled receptors having homology to the p2y
purinoreceptor 1 (p2y1)
Patent: EP 1219638-A 1.03-JUL-2002;
Pfizer Limited (GB); Pfizer Inc. (US)

FEATURES
source
1. 1014
Location/Qualifiers

BASE COUNT 259 a 263 c 188 g 304 t
ORIGIN

Query Match 100.0%; Score 1014; DB 6; Length 1014;
Best Local Similarity 100.0%; Pred. No. 8.7e-258;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	961	GTAAGCGGGAACCTTTGAGCAAGCAAGAAATTTAGTTACTCAAAACACCTTGA	1014
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LOCUS	AXI48186	1014 bp	DNA
DEFINITION	Sequence 27 from Patent WO0136471.	linear	PAT 08-JUN-2001
ACCESSION	AXI48186		
VERSION	AXI48186.1	GI:14347086	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	Chen, R., Dang, H.T. and Lowitz, K.P.		
AUTHORS	Endogenous and non-endogenous versions of human g protein-coupled		
TITLE	receptors		
JOURNAL	Patent: WO 0136471-A 27 25-MAY-2001;		
FEATURES	Arena Pharmaceuticals, Inc. (US)		
source	Location/Qualifiers		
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BASE COUNT	258 a 263 c 189 g 304 t		
ORIGIN			
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Best Local Similarity	99.9%; Pred. No. 2.3e-257;		
Matches 1013; Conservative 0; Mismatches 1; Indels ~ 0; Gaps 0;			
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Db	61	TTTGGAAATTCACATGATGAAGAAATCCCACTCAAGATGACATCTCCCTGTTATTTAT	120
Qy	121	GGCATATCTTCCCTGCTGGGGAATTCOCAGGCAATGCAGTAGTGATATCCATTTACATTTTC	180

Db	121	GGCATTTATCTTCCTCGGAGGATTTCCAGGCAATGACATAGATATCCACTTACATTTTC	180
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QY	421	TGCTTTTCATTCACAAACATCTCATATGTGCAGTTTATACCTCTGCTGTGTGTGATCATTT	480
Db	421	TGCTTTTCATTCACAAACATCTCATATGTGCAGTTTATACCTCTGCTGTGTGTGATCATTT	480
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QY	961	GTAAGCGGGAACCTTGTAGCAAGCAAAAGAAATTAAGTACTCAAAACAAACCTTTGA	1014
Db	961	GTAAGCGGGAACCTTGTAGCAAGCAAAAGAAATTAAGTACTCAAAACAAACCTTTGA	1014
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
ORGANISM			
SOURCE			
REFERENCE			
AUTHORS			
1			
Wei, M. H., Zhao, Q. C., Cravchik, A. C., di Francesco, V. C. and			

Db 481 TCACGTGAGTCTGTCATTCCTCCGATGACCTCTCTGTGATCATCAACCAACAGACCAACAGA 540

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Db 961 ATTTTGTGACCACTGACCTGCGATGGAATCACTAATTAAGTGTACAACTG 1014

RESULT 6
AB083598 1014 bp DNA linear PRI 24-MAY-2002
LOCUS AB083598 Homo sapiens GPCR gene for putative G-protein coupled receptor.
DEFINITION complete cds, clone:hGPCR16.
ACCESSION AB083598
VERSION AB083598.1 GI:20152259
KEYWORDS
SOURCE Homo sapiens DNA, clone:hGPCR16.
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Takeda, S., Kadowaki, S., Haga, T., Takaesu, H. and Mitaku, S.
AUTHORS Identification of G protein-coupled receptor genes from the human genome sequence
TITLE
JOURNAL
REFERENCE 2 (bases 1 to 1014)
AUTHORS Takeda, S., Kadowaki, S., Haga, T., Takaesu, H. and Mitaku, S.
TITLE Direct Submission
JOURNAL Submitted (10-APR-2002) Shigeaki Takeda, Gunma University, Department of Biological and Chemical Engineering, Faculty of Engineering, 1-5-1, Kiryu, Gunma 376-8515, Japan
(E-mail:stakeda@bce.gunma-u.ac.jp, Tel:+81-277-30-1434, Fax:+81-277-30-1434)
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BASE COUNT 258 a 263 c 189 g 304 t
ORIGIN
Query Match 99.8%; Score 1012.4; DB 9; Length 1014;
Best Local Similarity 99.8%; Pred. No. 2.3e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGATGAGCCACTAGACTATTTAGCAAAATGCTTGATTTCCCGATATGACGCTG 60
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RESULT 7
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LOCUS Homo sapiens G protein-coupled receptor (GPR80) gene, complete cds.
DEFINITION AF411109
ACCESSION AF411109.1 GI:16566322
VERSION
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1014)
AUTHORS Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vantti,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
TITLE Discovery and mapping of ten novel G protein-coupled receptor genes
JOURNAL Gene 275 (1), 83-91 (2001)
MEDLINE 21458555
PUBMED 11574155

REFERENCE 2 (bases 1 to 1014)
AUTHORS Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vantti,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
TITLE Submitted (17-AUG-2001) Department of Pharmacology, University of
JOURNAL Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada
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BASE COUNT 258 a 263 c 189 g 304 t

Query Match 99.8%; Score 1012.4; DB 9; Length 1014;
Best Local Similarity 99.9%; Pred. No. 2.3e-257;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 961 GTAAAGCGGGAACCTTGTAGCAAGCAAAATTTAGTTACTGCAAAACACCTTGA 1014
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RESULT 8
AX458238 1081 bp DNA linear PAT 08-JUL-2002
LOCUS AX458238
DEFINITION Sequence 1 from Patent W00246414.
ACCESSION AX458238
VERSION AX458238.1 GI:21724972
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1

AUTHORS Ramanathan, C., Feder, J., Nelson, T., Cacace, A., Barber, L. and Ryssek, R. P.
 TITLE A novel human g-protein coupled receptor, hgrp1my23, expressed highly in kidney
 JOURNAL Patent: WO 0246414-A 1 13-JUN-2002;
 Bristol-Myers Squibb Company (US)
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 Wittenberger, T., Hellebrand, S., Munc, A., Kretschmann, H. J.,
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 GPR99, a new G protein-coupled receptor belonging to a new subgroup
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Best Local Similarity 99.98; Pred. No. 2.3e-257;
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JOURNAL    Suwa, M., Sato, T., Okouchi, I., Arita, M., Futami, K., Matsumoto, S.,
REFERENCE  Tsutsumi, S., Aburatani, H., Asai, K. and Akiyama, Y.
AUTHORS    Genome-wide discovery and analysis of human seven transmembrane
TITLE       helix receptor genes
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 1414)
AUTHORS    Suwa, M.
TITLE       Direct Submission
JOURNAL    Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research
REFERENCE  Center (CBRC), National Institute of Advanced Industrial Science
AUTHORS    and Technology (AIST), 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan
TITLE       (E-mail: m-suwa@aist.go.jp, URL: http://www.cbrc.jp/,
JOURNAL    Tel: 81-3-3599-8080, Fax: 81-3-3599-8081)
COMMENT    This sequence is a seven transmembrane helix receptor candidate
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           transmembrane helix prediction.
           And the sequence is submitted by the collaborative project between
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 1 Wei, M.H., Zhao, Q.C., Cravchik, A.C., di Francesco, V.C. and
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 TITLE Isolated human g-protein coupled receptors, nucleic acid molecules
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JOURNAL Skuce, C.
TITLE Direct Submission
COMMENT Submitted (27-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
Ch10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Sep 28, 2001 this sequence version replaced gi:15808158.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; Sw,
SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information on the WormPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone confis of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
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of Pieter de Jong. For further details see
http://www.chori.org/dacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
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Db 4611 TCATGTTAGCTGTATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 4552
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Db 4551 TCACCTGTTGCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCT 4492
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Db 4311 AGGCTAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4252
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Db 4251 CATTGACCTTAATCATGCTTTCTAGACATTAAGCTGCTGTAACACCTTTGTAACCTGTTA 4192
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Db 4191 CTATATGTGTGTGTCAGCAGCACTTTCAGCAGGCTGTCTCTCAACAGTATGATGCAAA 4132
QY 961 GTAGCGGGAACCTTGAGCAAGCAAAATTTAGTTACTCAACACCTTTGA 1014
Db 4131 GTAGCGGGAACCTTGAGCAAGCAAAATTTAGTTACTCAACACCTTTGA 4078

RESULT 13
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 DEFINITION AC026756
 AC026756.15 GI:13112251
 VERSION HTG.
 KEYWORDS Homo sapiens.
 SOURCE Homo sapiens.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 156555)
 AUTHORS Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federpsiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Wilhelmy, J., Yu, S. and Davis, R.W.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 156555)
 AUTHORS Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federpsiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Yu, S. and Davis, R.W.
 JOURNAL Direct Submission
 TITLE Submitted (23-MAR-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
 REFERENCE 3 (bases 1 to 156555)
 AUTHORS Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federpsiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Lam, B., Mao, J., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Wilhelmy, J., Yu, S. and Davis, R.W.
 JOURNAL Direct Submission
 TITLE Submitted (23-FEB-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
 COMMENT On Feb 23, 2001 this sequence version replaced gi:12745089.
 ----- Genome Center
 Center: Stanford DNA Sequencing and Technology Development Center
 Center code: SDSTDC
 Web site: <http://sequence-www.stanford.edu/group/human/>
 Contact: hum-info@sequence.stanford.edu
 ----- Project Information
 Center project name: 870
 Center clone name: RP11-286P8
 ----- Summary
 This sequence was finished as follows unless otherwise noted:
 all regions were double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
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 Best local Similarity 99.9%; Pred. No. 27e+257;
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 DB 140188 ATGATGAGCCACTAGACTATTATAGCAAAATGCTTGTGATTTCCCGATTATGACAGTCTGT 140247

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 DB 140368 AAAATGAGACCTTGGAAAGAGCAGACACATCATTTATGCTTAACCTGGCTGCACAGTCTG 140427
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 DB 140428 CTTGATCTGACAGACCTCCCTCCCTGATTCATCTACTATGCGAGTGGGAAAACTGGATTC 140487
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 DB 140548 ATCCCTCTTCTCACTGCTGTTTCAAGCATCTTCCGCTACTGTGTATCATTTACCCATGAC 140607
 QY 421 TCGTTTTCATTCACAAACCTGATGATGAGTTGAGTTCGCTGCTGCTGGTGGATCATTT 480
 DB 140608 TCGTTTTCATTCACAAACCTGATGATGAGTTGAGTTCGCTGCTGCTGGTGGATCATTT 140667
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 DEFINITION Sequence 2 from Patent WO0149847.
 ACCESSION AX191332
 VERSION AX191332.1 GI:15209582
 KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Glucksman, M.A. and White, D.
TITLE 26904, 38911, and 39404, seven-transmembrane proteins / g-protein coupled receptors
JOURNAL Patent: WO 0149847-A 2 12-JUL-2001;
Millennium Pharmaceuticals, Inc. (US)
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BASE COUNT 461 a 403 c 302 g 563 t
ORIGIN

Query Match 99.7%; Score 1010.8; DB 6; Length 1729;
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Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION Sequence 85 from Patent WO0136473.
ACCESSION AX147840
VERSION AX147840.1 GI:14346841
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Vogel, G., Wood, L.S., Parodi, L.A., Hiebsch, R.R., Lind, P., Slightom, J., Schellin, K.A., Kayles, P.S., Bannigan, C.M., Ruff, V., Seglitz, T., and Huff, R.M.
TITLE Novel g-protein-coupled receptors
JOURNAL Patent: WO 0136473-A 85 25-MAY-2001;
PHARMACIA & UPJOHN COMPANY (US)
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Job time : 2796 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 13:40:53 ; Search time 81 Seconds
(without alignments)
857.258 Million cell updates/sec

Title: US-10-023-775B-2

Perfect score: 1771

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
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- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	556.5	31.4	361	13 Q90X57	Q90X57 xenopus lae
4	547	30.9	374	13 Q57466	Q57466 melalegris g
5	479	27.0	330	4 Q9BXA5	Q9BXA5 homo sapien
6	479	27.0	334	4 Q9BXA5	Q9BXA5 homo sapien
7	445.5	25.2	309	11 Q8R528	Q8R528 mus musculu
8	421	23.8	328	11 Q9ERK9	Q9ERK9 mus musculu
9	418	23.6	317	11 Q99WT6	Q99WT6 mus musculu
10	399	22.5	369	4 Q90Q06	Q90Q06 homo sapien
11	390.5	22.0	399	11 Q8R311	Q8R311 mus musculu
12	369	20.8	359	13 Q90Z22	Q90Z22 oncorhynch
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14	359	20.3	347	6 Q9MZM1	Q9MZM1 eulemur mac
15	359	20.3	347	6 Q9MZM0	Q9MZM0 perodicticu
16	357	20.2	347	6 Q9MZP6	Q9MZP6 presbytis j

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22	356	20.1	347	6 Q9MZP9	Q9MZP9 nasalis lar
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26	356	20.1	347	6 Q9MZP3	Q9MZP3 presbytis e
27	356	20.1	347	6 Q9MZP2	Q9MZP2 mandrillus
28	356	20.1	347	6 Q9MZP0	Q9MZP0 macaca assa
29	356	20.1	347	6 Q9MZP9	Q9MZP9 macaca arc
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ALIGNMENTS

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AC Q96P68; ID Q96P68; 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE G protein-coupled receptor (Putative G-protein coupled receptor).

GN GPR80 OR GPCR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

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RP SEQUENCE FROM N.A.

RX MEDLINE-21458557; PubMed-11574155;

RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arhltko O.,

RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;

RT "Discovery and mapping of ten novel G protein-coupled receptor

RT genes.";

RL Gene 275:83-91(2001).

RN [2]

RP SEQUENCE FROM N.A.

RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;

RT "Identification of G protein-coupled receptor genes from the human

RT genome sequence.";

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF411109; AL26480.1; -;

DR EMBL; AB083598; BAB89311.1; -;

DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; 7tm_1; 1.

DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.

RP Receptor.

SO SEQUENCE 337 AA; 38251 MW; 6814EA0044756CE6 CRC64;

Query Match 100.0%; Score 1771; DB 4; Length 337;

Best Local Similarity 100.0%; Pred. No. 1.8e-159;

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QY 1 MNEPLDIANASDPDYAAAFGCTDENIPKMHYIYIYIIFLVGPGNAVITYIE 60
DB 1 MNEPLDIANASDPDYAAAFGCTDENIPKMHYIYIYIIFLVGPGNAVITYIE 60
QY 61 KMRPKSSTIIMLACTDLYLTSPLFIHYVAGENWIRGDMCKFIRESFHNLYSS 120
DB 61 KMRPKSSTIIMLACTDLYLTSPLFIHYVAGENWIRGDMCKFIRESFHNLYSS 120
QY 121 ILFLTCFSIFRYCVIIHPMCSFISIKTRCAVAVVAVIISLVAVIPMTFLITSTNR 180
DB 121 ILFLTCFSIFRYCVIIHPMCSFISIKTRCAVAVVAVIISLVAVIPMTFLITSTNR 180
QY 181 SACLDLTSDELNTIKYINLITATTCPLPIVITLTCTTIHHTLHGLQDSCLOKAR 240
DB 181 SACLDLTSDELNTIKYINLITATTCPLPIVITLTCTTIHHTLHGLQDSCLOKAR 240
QY 241 RLTIILLAFYVCLPFIHILRVIRIESRLSISCSINQHEAVISRPALALMTFG 300
DB 241 RLTIILLAFYVCLPFIHILRVIRIESRLSISCSINQHEAVISRPALALMTFG 300
QY 301 LYVVSDFNFQAVCSIVRCVSGNLEQAKKISYSNNP 337
DB 301 LYVVSDFNFQAVCSIVRCVSGNLEQAKKISYSNNP 337
```

RESULT 2

```
Q9DE05 PRELIMINARY; PRT; 357 AA.
ID Q9DE05
AC Q9DE05;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE p2y receptor.
OS Raja erinacea (little skate).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hynostomales; Pristigastera; Batoidae;
OC Rajiformes; Rajidae; Raja.
OC NCBI_TaxID=7782;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=20459151; PubMed=10900200;
RA Dranoff J.A., O'Neill A.F., Franco A.M., Cai S.Y., Connolly G.C.,
RA Ballatori N., Boyer J.L., Nathanson M.H.;
RT "A primitive ATP receptor from the little skate Raja erinacea."
RL J. Biol. Chem. 275:30701-30706(2000).
DR EMBL: AF242850; AAC42684.1;
DR HSSP: P34996; 1DD.
DR InterPro: IPR00276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 357 AA; 41239 MW; 14604E15DCBDA1 CRC64;
```

Query Match 32.6%; Score 577.5; DB 13; Length 357;
Best Local Similarity 37.3%; Pred. No. 1.4e-46;
Matches 117; Conservative 59; Mismatches 121; Indels 17; Gaps 5;

```
QY 13 DFDYDAAAFGNCND-----ENTPLKMHYIPVYIGIIFLVGFGNAVITYIEFKM 62
DB 5 DFDYDAAAFGNCND-----ENTPLKMHYIPVYIGIIFLVGFGNAVITYIEFKM 62
QY 63 RPKSSTIIMLACTDLYLTSPLFIHYVAGENWIRGDMCKFIRESFHNLYSS 122
DB 63 RPKSSTIIMLACTDLYLTSPLFIHYVAGENWIRGDMCKFIRESFHNLYSS 122
QY 123 FLTCFSIFRYCVIIHPMCSFISIKTRCAVAVVAVIISLVAVIP-MTFLITSTNR 181
DB 123 FLTCFSIFRYCVIIHPMCSFISIKTRCAVAVVAVIISLVAVIP-MTFLITSTNR 181
QY 182 ACIDLTSDELNTIKYINLITATTCPLPIVITLTCTTIHHTLHGLQDSCLOKAR 240
DB 182 ACIDLTSDELNTIKYINLITATTCPLPIVITLTCTTIHHTLHGLQDSCLOKAR 240
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DB 185 TCYDPTSKELLETFYITSMSTFFGFCIPATILVCGFYIKALISDMKTP--LRKSV 242
QY 241 RLTIILLAFYVCLPFIHILRVIRIESRLSISCSINQHEAVISRPALALMTFG 297
DB 243 RLVIIVAVPAISILPFIHVKMKNLQSRILYQGLDTCGMNRRVATQVTRGLASLNSCV 302
QY 298 NLLLYVVSDFNFQ 311
DB 303 DPLIYFLAGDFFRR 316
```

RESULT 3

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Q90X57 PRELIMINARY; PRT; 361 AA.
ID Q90X57
AC Q90X57;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE p2y1 nucleotide receptor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheng A.W., Tsai K.W.;
RT "Cloning of Xenopus p2y1 Receptor."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF432354; AAL27614.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 361 AA; 41002 MW; E5B2D605F5B57BED CRC64;
```

Query Match 31.4%; Score 556.5; DB 13; Length 361;
Best Local Similarity 35.2%; Pred. No. 1.4e-44;
Matches 113; Conservative 70; Mismatches 123; Indels 15; Gaps 4;

```
QY 22 GN--CNDENIPKMHYIPVYIGIIFLVGPGNAVITYIEFKMRPKSSTIIMLACT 78
DB 25 GNWTKCCLRTGTFQFYIIPVYIVCTGIGNSVALMTFHKRPMSSISVYMFNALA 84
QY 79 DLVLTSPLFIHYVAGENWIRGDMCKFIRESFHNLYSSIFLTCFSIFRYCVIIHP 138
DB 85 DLVLTSPLFIHYVAGENWIRGDMCKFIRESFHNLYSSIFLTCFSIFRYCVIIHP 144
QY 139 MSCFSIKTRCAVAVVAVIISLVAVIPMTFLITSTNRNRS-ACIDLTSDELNTIKW 197
DB 145 LKSLGRLLKRNKSIYISALVWFIYAGISPLIFSGTGRKNTTTCDFSSDEYLRSYFI 204
QY 198 YNLIATTCPLPIVITLTCTTIHHTLHGLQDSCLOKARLTIILLAFYVCLP 257
DB 205 YSMCTVFGCIPILILGCGYGLVRLIKDMNNAFLRKRSIYIVITVAVASLP 264
QY 258 HILVIRIESRLSISCSINQHEAVISRPALALMTFGNLLYVVSDFNFQAVC 314
DB 265 HVKKNLNLRLRDLQSPKCNFNDRVATQVTRGLASLNSCVDPILYFLAGD 319
QY 315 STVRCVSGNLEQAKKISYSN 335
DB 320 ---RRKLSRATRRKASRSEAN 337
```

RESULT 4

```
Q57466 PRELIMINARY; PRT; 374 AA.
ID Q57466
AC Q57466;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
```

DR HSSP: P34996: 1DD0.
DR InterPro: IPR000276: GPCR_Rhodpsn.
DR Pfam: PF00001: 7tm_1: 1.
DR PRINTS: PR00237: GPCR_RHODPSN.
DR PROSITE: PS00237: G-PROTEIN_RECEP_FL_1: 1.
DR PROSITE: PS50262: G-PROTEIN_RECEP_FL_2: 1.
DR G-protein coupled receptor: Glycoprotein: Receptor: Transmembrane.
KW SEQUENCE 330 AA; 38283 MW; 6D3C70E340866BAB CRC64;
SQ
Query Match 27.0%; Score 479; DB 4; Length 330;
Best Local Similarity 35.9%; Pred. No. 2.7e-37;
Matches 110; Conservative 61; Mismatches 123; Indels 12; Gaps 6;
QY 23 NCTDEN-----IPKMHYLPVYIGIIFLPGFGNAVYISTYIFKMRPKSSTIIMLNAC 77
DB 4 NATCKNMLAAEAALEKYYLSIFGIIEFVGVLGNTIVYGYIFSLKMNSSNLYLFNLSV 63
QY 78 TDLIYLSLPELHIYVASEGWMIFGDFMCKIFRFSFHNLSILFLCFSIFRCVITH 137
DB 64 SDLAFLCTLPMLINSYANG-NMIYGDVLCISNRVYLANLTSILFLFISIDRLTIKY 122
QY 138 PMSCFSIHKTRCAYAVCAVWIIISLVAVIPTFLITSTNRNRSACDLTSSDELNTIKW 197
DB 123 PFRRHLQKKFEALISLAIWLVLTLEPLILPLINPVITDNGTCDNFASGDPNVLII 182
QY 198 YNLITATATFCLPLVITYLTCTTY-INTLHGLODSCLR-QKRRRLTILLAFYCFE 255
DB 183 YSMCLTTLGLGFIPLFVWCFFYKLTALFLKORNRQVATLPLEKPLNTVIMAVVLEFSLFT 242
QY 256 PFHLIYRIETRSLLS---ISCSITENOIHEAYISRPALATFNGLLIYVVDGNPQQA 312
DB 243 PIYHWRNRVRLASRLGSMKQYQCT-QVYINSYITVTRPLAFNSVINPVYFLLGDHFRDM 301
QY 313 VCSFTR 318
DB 302 LMGQLR 307
RESULT 6
Q8TDO8 PRELIMINARY; PRT; 334 AA.
AC Q8TDO8:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE P2Y purinoceptor 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Li N., Man T., Cao X.;
RT "Human P2Y purinoceptor 1.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR AF247785; AAL95690.1;
SQ SEQUENCE 334 AA; 38697 MW; 33146E1AD87F0E81 CRC64;
Query Match 27.0%; Score 479; DB 4; Length 334;
Best Local Similarity 35.9%; Pred. No. 2.7e-37;
Matches 110; Conservative 61; Mismatches 123; Indels 12; Gaps 6;
QY 23 NCTDEN-----IPKMHYLPVYIGIIFLPGFGNAVYISTYIFKMRPKSSTIIMLNAC 77
DB 8 NATCKNMLAAEAALEKYYLSIFGIIEFVGVLGNTIVYGYIFSLKMNSSNLYLFNLSV 67
QY 78 TDLIYLSLPELHIYVASEGWMIFGDFMCKIFRFSFHNLSILFLCFSIFRCVITH 137
DB 68 SDLAFLCTLPMLINSYANG-NMIYGDVLCISNRVYLANLTSILFLFISIDRLTIKY 126
QY 138 PMSCFSIHKTRCAYAVCAVWIIISLVAVIPTFLITSTNRNRSACDLTSSDELNTIKW 197
DB 127 PFRRHLQKKFEALISLAIWLVLTLEPLILPLINPVITDNGTCDNFASGDPNVLII 186

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0Y 198 INLILFATPECCPLVIVITLCYTTI-ITHLTHGQTPSCAK-QARRLTILLALFYVCEL 255
Db 187 YSMCLTILGFLPLPEMCFEYKIAFLFKORNRQVATAPALEKPLNIVIAVVFSLFT 246
0Y 256 PEHLIRVIRIESRLTS--ISCSIQIHEAVIVSRPLAALNFQNLILVYVSDNQQA 312
Db 247 PYHVARNRIASRLSGSMQYOCT-QVIVINSFYIVTRPLAFNSVINPVEFYLLGDHFRDM 305
0Y 313 VCSFVR 318
Db 306 LMANQLR 311

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RESULT 7
OBR528
ID OBR528: PRELIMINARY; PRT; 309 AA.
AC OBR528:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cysteinyl leukotriene 2 receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute-
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
NCBI_TaxId=10090;
[1]
NM SEQUENCE FROM N.A.
RN RP Ishii S.;
RA "Mouse CysLT2 Gene.";
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases
RL EMBL; AB058930; BAB86881.1; -.
DR
KW Receptor.
SQ SEQUENCE. 309 AA; 35226 MW; 96FACCB8BAF96974 CRC64;

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RESULT 8	
09ERK9	
ID	PRELIMINARY:
AC	PRT: 328 AA.
09ERK9:	
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	P276 receptor (Hypothetical 36.7 kDa protein).
OS	Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVEV;
RX MEDLINE=21160052; PubMed=11259526;
RA Lazarowski E.R., Rochelle L.G., O'Neal W.K., Bouchet C.M.P.,
RA Grubb B.R., Zhang V., Harden T.K., Boucher R.C.,
RT "Cloning and functional characterization of two murine uridine
RT nucleotide receptors reveal a potential target for correcting ion
RT transport deficiency in cystic fibrosis gallbladder.";
RL J. Pharmacol. Exp. Ther. 297:43-49(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBD databases.
DR EMBL; AF298899; AAG24619.1; -
DR EMBL; BC027331; AAH27331.1; -
DR HSSP; P3496; 1DDO.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PF00237; GPCRHHODPSN.
DR PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.
KM Hypothetical protein, Receptor.
SO SEQUENCE 328 AA; 36721 MW; 00F9DF5ADAF903E CRC64;

RESULT	9
ID	099MT6
AC	099MT6
DT	01-JUN-2001 (TrEMBLrel, 17, Created)
DT	01-JUN-2001 (TrEMBLrel, 17, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
DE	G-protein coupled receptor GPR31.
GN	GPR31.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SPRAIN=C57BL.
RX	MEDLINE=21172992; PubMed=11273702;
RT	Wittenberger T., Schaller H.C., Hellebrand S.;
RT	"An expressed sequence tag (EST) data mining strategy succeeding in
RT	the discovery of new G-protein coupled receptors."
BL	J. Mol. Biol. 307:799-813(2001).

DR EMBL: AF295367; AAK01867.1; -
 DR HSSP: P34996; 1DD.
 DR MGD: MG1:1934135; GP-91.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
 DR Receptor.
 SQ SEQUENCE 317 AA; 36701 MW; 4E22F0608F928B36 CRC64;

Query Match 23.6%; Score 418; DB 11; Length 317;
 Best Local Similarity 33.7%; Pred. No. 1.5e-31;
 Matches 99; Conservative 58; Mismatches 127; Indels 10; Gaps 6;

QY 31 LKMHLYPIVYIGIIFLVGFGNAVISTYIFKMRPKSSITIMLNACTDLYLPSFLI 90
 DB 17 LKRYLSAFYAEFEFGLGNTVYVGYLFCKMKNNSNVYLFENLISDFAEFLCPLI 76
 QY 91 HYVASENMFQDFMCKFRFSFHFNLYSILFLCFISFRVCVLIHPMCSFISHTKCA 150
 DB 77 KSYAN-DKGTGVDLCISNRVYVHTNLTSMILLIYISMDRLIMKYPREHFLQKKEFA 135
 QY 151 VVACAVVWIIISLVAVIPMTFLITSNRTNRSACLDLTSS--DELNTIKWYNLITATTEC 208
 DB 136 ILISLAVMALVTLVPLMTLFTINSYVKEGSGNCIDYASGNEPHNLI--YSICLTLGLFL 193
 QY 209 LELVIVTLCYTTIHTLHTGLQTDSC--KOKARLTILLALFYVCFPHILVRIE 266
 DB 194 IELVWCFEYKRVVFLKRRSQQAFLDPLDKPRLVAVVIFSLFPPYHMRMLRIA 253
 QY 267 SRLLS--ISCSIEINOIHEAVISRPPLAINTFGNLLYVVSDFNOQAACSTVR 318
 DB 254 SRLDSHPOGCT-QKAIKSITYITLTPPLAFINSAINPLFTYLMGDHTEMILSKFR 306

RESULT 10
 ID 09U006 PRELIMINARY; PRT; 369 AA.

AC 09U006; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DE 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Chemokine receptor CCR9 (CC chemokine receptor 9A).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9248139; PubMed-10229797;
 RA Zaballo A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
 RT Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
 RT receptor for the chemokine TECK.
 RL J. Immunol. 162:5671-5675(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yu C.-R., Peden K.W.C., Farber J.M.;
 RT "CCRG and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckbeta-
 RT 15)."
 RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AJ133337; CAB43477.1;
 DR InterPro: IPR004069; CC_Chemkin9.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PR01558; CHEMOKINER1.
 DR PRINTS: PR01531; CHEMOKINER9.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
 DR PROSITE: PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
 DR Receptor.
 KW

SQ SEQUENCE 369 AA; 42015 MW; F27CEADCF66B44C CRC64;

Query Match 22.5%; Score 399; DB 4; Length 369;
 Best Local Similarity 29.1%; Pred. No. 1.1e-29;
 Matches 104; Conservative 70; Mismatches 145; Indels 38; Gaps 11;

QY 4 PLDYLANASDPFDYAAAFGN-----CTDENI-PLKMHLYPIVYIGI 44
 DB 3 PIDEF---TSPINMADYSESTSSMEDVYVNFDFCEKNVNRGFASHFLPPLWLVF 59
 QY 45 LVGFPGNAVISTYIFKMRPKSSITIMLNACTDLYLPSFLIHYVASENMFQDF 104
 DB 60 IYGALGNSIVIIYVWYCTRYKMTDFLLNLAIADLLFLVTLPEFA--IAADQWFQTF 117
 QY 105 MCKFRFSFHFNLYSILFLCFISFRVCVLIHPMCSFISHTKRC--AVACAVWIIISL 162
 DB 118 MCKVNSMVKMNFYSVLLIMCISDRYALIAQAMRAHWRERLLYSKVCFTIWLVA 177
 QY 163 VAVIPMTFLITSNRTNRSACLDLTSSDELNTIKWYNLITATTE--FCLPLVIVTLCY 219
 DB 178 ALICIPILXSQIKESGIALCMVYPSDESTKTK--SAVLTILVILGFLPFLVMACTT 235
 QY 220 TIIHTLHTGLQTDSCIKOKARLTILLALFYVCFPHILVRIE-ILVRIEISRLSIS-CSIE 277
 DB 236 ITHHTL---IOAKSSKHKALKVTLVTLVFLVSCPPYNCILLVOTIDAYAMFISNCAVS 292
 QY 278 NOIHEAVISRPPLAINTFGNLLYVVSDFNOQAACSTVRVRCVSGNLQAKKISYS 334
 DB 293 TINDICEVYOTIAPHSCLNPVLYVGEVRRRDLVKTL--KNLCISQAOQWVSPT 347

RESULT 11

ID 08R311 PRELIMINARY; PRT; 399 AA.

AC 08R311; 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, last sequence update)
 DE 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Coagulation factor II (thrombin) receptor-like 1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC025432; AAH25432.1;
 KW Receptor.
 SQ SEQUENCE 399 AA; 44679 MW; 807C79464AB9B3EF CRC64;

Query Match 22.0%; Score 390.5; DB 11; Length 399;
 Best Local Similarity 29.9%; Pred. No. 7.6e-29;
 Matches 97; Conservative 65; Mismatches 129; Indels 33; Gaps 9;

QY 35 YLPVYIGIIFLVGFGNAVISTYIFKMRPKSSITIMLNACTDLYLPSFLIHYXA 94
 DB 79 FLPVYIIVVIGLPSNGMALWIFLRTKKHPAVIYMANLADLSVIMPLATAYHL 138
 QY 95 SGNMIFQDFMCKFRFSFHFNLYSILFLCFISFRVCVLIHPMCSFISHTKCAVAVAC 154
 DB 139 HGNMNVYGGALCKVLGIFYGNMYCSILMTCLSVGRVAVYNPKG---HRRKANIV 194
 QY 155 AV---VWISLVAVIVP-----TFLITSNRTNRSACLDLTSSDEL-NTIKWYNLITAT 205
 DB 195 GVSALWILFLVTLPIPLVYMKOTIYIPALNIT---TCHVLDPEVLVGMFVFLSLAG 251
 QY 206 TFCPLVIVTLCYTTIHTLHTGLQTDSC--KOKARLTILLALFYVCFPHILVRIE 263
 DB 252 VLEFPAITLASAVILKTLRSGADHESEKROKRIILITVILAMVYCFAPSNLLVAV 311
 QY 264 RIESRLSISCSIEINOIHEAVISRPPLAINTFGNLLYVVSDFNOQA-----AVCSTVR 318

Db 312 ----HFLLIKTOROSHYALYLALCLSTLNSCIDPFVYFVSKDFRDHARNALLCSVR 367
 QY 319 -----CKVSGNLEQAKKISYSNN 336
 Db 368 TVNMQISTSSNKRKSGSYSSS 391

RESULT 12

Q90222 PRELIMINARY; PRT; 359 AA.
 AC Q90222;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE IL-8 receptor.
 GN IL-8.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang H., Thorgaard G.H., Ristow S.S.;
 RT "Molecular cloning and genomic structure of an interleukin-8 receptor-
 like gene from a homozygous clones of rainbow trout (Oncorhynchus
 mykiss).";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF260964; AKA48500.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_FL_2; 1.
 KM Receptor.
 SQ SEQUENCE 359 AA; 39981 MW; A92A9038AAC97B7B CRC64;

Query Match 20.8%; Score 369; DB 13; Length 359;
 Best Local Similarity 30.3%; Pred. No. 7.5e-27;
 Matches 105; Conservative 62; Mismatches 136; Indels 44; Gaps 13;

QY 1 MNEPLDYLANASDFPDYAAA-----FGNCTDENI-----PLKMHYLPVYIGII 43
 Db 1 MFEVLVDYKA-DY-DKXANDSYFNTSPDLNFDLSCAQLSGAVIFLCVLAIV 58
 QY 44 FLVGFEGNAVYISTYIFKMRPKMSSTIMLNACTDILLYLSPELIIHYASG--ENWIF 101
 Db 59 FLAVVGNLTVGLVIGFSQOSLTPSDVYLFHLTVADGLALTLPF---WAANTLHGMI 114
 QY 102 GDMCKFRIRSFHFNYSILFLCFSEIFRYCVIIHMSGFSIHKTRCAVYACAVYIIS 161
 Db 115 GDFLCKFLSLVMEASFYSLFLVCLISVDRIYIVPAKSRKGRACRMVACTFTWTLG 174
 QY 162 LVAVIEMPTFLITST-NRTNSAC---DLTSSD--ELNTIKWNLITATFCLPIVI 215
 Db 175 GALSPLALFNDATPQGGPTPCAENHDDLSATHWRLATGRLIIL-----GFLPLVIMV 230
 QY 216 LCYTTIIHVL--THGLQDSCLOKARRLTILLAFYCVFLPPH--ILNVIRESPLS 271
 Db 231 ACYSIVYARLQTHGEQ----KRRARVYIAVFAFLCMTPLHMTVMADTLIRAKLVR 285
 QY 272 ISGSIENQIHNAVYSRPLAAMTFGLLIYVVSDFQAVGCVSTR 318
 Db 286 FDCAVRRVDLALQVTHSLALVHSFVNPVLYAFVGEKFRGNLALVR 332

RESULT 13

Q9NOMO PRELIMINARY; PRT; 358 AA.
 AC Q9NOMO;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE GCR3 receptor.

OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wolfe G.C., Mudgett J.S.;
 RT "Cloning and characterization of the sheep GCR3 receptor."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF265468; AAF71786.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_FL_2; 1.
 KM Receptor.
 SQ SEQUENCE 358 AA; 40985 MW; 2B54F9128590181E CRC64;

Query Match 20.3%; Score 359.5; DB 6; Length 358;
 Best Local Similarity 28.2%; Pred. No. 5.9e-26;
 Matches 84; Conservative 63; Mismatches 144; Indels 7; Gaps 5;

QY 16 DYAAAFGNCIDENI-PLKMHYLPVYIGIIFLVGPPGNAVYISTYIFKMRPKMSSTIMLN 74
 Db 21 DYEGAL-PCERSNVEKLAQFLPLYSLVEMIGLVNVAVVVILTKRKRLRMINTNYL 79
 QY 75 LACTDILLYLSPELIIHYASGENWIFGDMCKFRIRSFHFNYSILFLCFSEIFRYCV 134
 Db 80 LAISDVLEFVTLPPWHI-YRRKMRKMGHMKLSLYMGLYSELFIITLIDYXIA 138
 QY 135 ITHMSEFSIHKTRCAVYACAVYIISLVAVIEMPTFLITSTNRTNSACIDLASSDELNT 194
 Db 139 IVHAVFLRARTVYFGLVTSIFTWGLAGLAALPEFFHEHFOEAGLTCSPLENNVNA 198
 QY 195 IKWYN-LITATFCLPIVLYTLCYTIITHTHGLQDSCLOKARRLTILLAFYVC 253
 Db 199 WKQPHALRMNIGLALPLVMAVCYSIGIITL--LCPKSKKAIKRLIFVIMVVFIF 255
 QY 254 FLPEHILVRIIESRLISCSISIENQIHNAVYSRPLAAMTFGLLIYVVSDFQAV 311
 Db 256 WTPFNLLVLLAFQNMHLETCDEOSRQDLAMLVETVIAIYHCCVNPYIAVFGERRFK 313

RESULT 14
 Q9WZM1 PRELIMINARY; PRT; 347 AA.

AC Q9WZM1;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Chemokine receptor CXCR4 (Fragment).
 GN CXCR4.
 OS Eulemur macaco (Pteropus macaco).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Strepsirrhini; Lemnidae; Eulemur.
 OX NCBI_TaxID=30602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zheng X.-Z., Zhang Y.-P., Geng Z.-C.;
 RT "Molecular Evolution of the Chemokine Receptor CXCR4 Gene Sequences in
 Primates.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AF172242; AAR89362.1;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR01558; CHEMOKINER11.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PRINTS: PR01568; LYMPHOTACTNR.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; 1.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 13:36:28 ; Search time 22 Seconds

(without alignments)
635.342 Million cell updates/sec

Title: US-10-023-775b-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANASDFPDYAAA.....RCKVSGNLEPAKKISNNP 337

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	575	32.5	373	1 P2YR_MOUSE	P49650 mus musculu
2	567	32.0	373	1 P2YR_HUMAN	P47900 homo sapien
3	565.5	31.9	362	1 P2YR_CHICK	P49652 gallus gall
4	565.5	31.9	362	1 P2YR_MELGA	P49651 rattus norv
5	565	31.9	373	1 P2YR_BOVIN	P48042 bos taurus
6	562	31.7	373	1 P2YR_XENTLA	P79928 xenopus lae
7	557	31.5	357	1 P2YR_HUMAN	P51582 homo sapien
8	514	29.0	361	1 P2YR_RAT	O35811 rattus norv
9	512	28.9	361	1 P2YR_MOUSE	O91547 mus musculu
10	503	28.4	361	1 P2YR_CHICK	O98907 gallus gall
11	492	27.8	368	1 CLT2_HUMAN	O98975 homo sapien
12	487.5	27.5	346	1 P2YR_MELGA	O93361 meleagris g
13	486.5	27.3	328	1 P2YR_RAT	P41232 rattus norv
14	483.5	27.0	374	1 P2YR_MOUSE	P41231 homo sapien
15	479	26.8	373	1 P2YR_HUMAN	O95n03 sus scrofa
16	474	26.0	377	1 CLT2_MOUSE	O92081 mus musculu
17	452	25.5	309	1 CLT2_MOUSE	O92081 mus musculu
18	442.5	25.0	309	1 CLT2_MOUSE	O92081 mus musculu
19	430	24.3	309	1 CLT2_MOUSE	O92081 mus musculu
20	423	23.7	328	1 P2YR_RAT	O63371 rattus norv
21	419.5	23.3	420	1 P2YR_HUMAN	P67749 xenopus lae
22	405	22.8	328	1 P2YR_MOUSE	O15077 homo sapien
23	404	22.8	430	1 P2YR_HUMAN	P30558 mus musculu
24	397	22.4	357	1 P2YR_HUMAN	P31666 homo sapien
25	396.5	22.4	432	1 P2YR_RAT	P66824 rattus norv
26	395.5	22.3	367	1 P2YR_MOUSE	O95n03 sus musculu
27	394.5	22.3	367	1 P2YR_HUMAN	O13304 homo sapien
28	391	22.1	428	1 P2YR_HUMAN	O00991 cricetus
29	389.5	22.0	425	1 P2YR_HUMAN	P56488 papio hama
30	388.5	21.9	425	1 P2YR_MOUSE	P55086 mus musculu
31	386.5	21.8	425	1 P2YR_HUMAN	P55116 homo sapien
32	383.5	21.7	397	1 P2YR_RAT	O63645 rattus norv
33	380	21.5	308	1 P2YR_CHICK	P32250 gallus gall

ALIGNMENTS

RESULT 1	ID	QUERY MATCH	STANDARD	PRT	AA
AC	P49650:				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).				
GN	P2RY1.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=129/Sv;				
RA	Leon C.;				
RT	"Thromboresistance in p2y1 receptor knockout mice."				
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS				
CC	ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECTS				
CC	OF EXTRACELLULAR ATP ON INSULIN SECRETION.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	entities requires a license agreement (See http://www.isb.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; U22829; AAA91302.1; -				P32249 homo sapien
DR	EMBL; AJ245636; CAB57317.1; -				P55085 homo sapien
DR	HSSP; P34996; 1DD.				P79960 xenopus lae
DR	MGI; MGI:105049; P2Y1.				P51677 homo sapien
DR	InterPro: IPR000276; GPCR_Rhodopsin.				O08675 mus musculu
DR	Pfam; PF00001; 7tm_1; 1.				O95n02 sus scrofa
DR	PRINTS; PR00237; GPCRHOOPS.				O92081 rattus norv
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.				O92468 rattus norv
DR	PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.				O99344 mus musculu
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.				O28474 macaca fasc
FT	DOMAIN 1				P56491 papio anubi
FT	TRANSNEM 53				P35407 rattus norv
FT	DOMAIN 75				
FT	TRANSNEM 88				
FT	DOMAIN 110				
FT	TRANSNEM 127				
FT	DOMAIN 147				
FT	TRANSNEM 127				

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FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 167 188 4 (POTENTIAL).
FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 266 285 6 (POTENTIAL).
FT DOMAIN 286 308 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 309 328 7 (POTENTIAL).
FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 374 402 BY SIMILARITY.
FT DISULFID 124 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42212 MW; 944125E9F4560B3 CRC64;

Query Match 32.5%; Score 575; DB 1; Length 373;
Best Local Similarity 36.5%; Pred. No. 6.3e-31;
Matches 109; Conservative 67; Mismatches 119; Indels 4; Gaps 2;

QY 24 CTDENIPDKMAYLVIIYGIIFLVCFPNNAVITYIFKMRPMKSTIIMLNACTDLIYL 83
DB 42 CALKRTGQFYLLAVYLIVFIIFLGNSVAIMFVFMKRMGSLVYMNALADPLIYV 101
QY 84 TSLPPLHYASGENWIFGDMCKFIRSFHFNYSSILFLTCSIFRYCVIIMHSCFS 143
DB 102 LTLFALLFYFNKTDWIFGDMCKKORFIHFVNLGSLFLTCSAHRSYGVVYPLKSLG 161
QY 144 IHRRCVAVACAVVMIISLVAVIMPTFLITSTNPNRS-ACGLDSSDELMTIKYNIL 202
DB 162 RLKKNALYVSVLVVAVVAVISPLFSGTGTRKNKVTQVTSNDLYNSYFLYSMCT 221
QY 203 TATFECPLVIVLYLCTYTIHTLHGLQTDSCLOKAKARLITLLAFYVCFELPHILRV 262
DB 222 TVAFECPLVILICGYGLIVAKALYNDLNSPLRKRKSYIVIVLYVFAVASYIFPHWKT 281
QY 263 IRISRL---LSISCSIEHQHEAYISRPALANTGNLLIYVVSDFQAVCSIVR 318
DB 282 MNLARLDFQTPENCDFNDRYATYQVYRGLASINSCVDPILYFLAGDTFRRRLRATR 340

RESULT 2
P2YR_HUMAN STANDARD; PRT; 373 AA.
ID P2YR_HUMAN STANDARD; PRT; 373 AA.
AC P47900;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2RY1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta; PubMed=8666290;
RX MEDLINE=96257237; PubMed=8666290;
RA Leon C., Vial C., Cazenave J.-P., Gachet C.;
RT "Cloning and sequencing of a human cDNA encoding endothelial P2Y1
RT purinoceptor."
RL Biochem. Biophys. Res. Commun. 218:783-788(1996).
RP SEQUENCE FROM N.A.
RX MEDLINE=96205320; PubMed=8630005;

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RA Janssens R., Commun D., Piroton S., Samson M., Parmentier M.,
RA Boeynaems J.M.;
RT "Cloning and tissue distribution of the human P2Y1 receptor.";
RL Biochem. Biophys. Res. Commun. 221:588-593(1996).
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Leon C., Vial C., Cazenave J.-P., Gachet C.;
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
RN 5;
RP SEQUENCE OF 95-373 FROM N.A., FUNCTION, AND INHIBITION STUDIES.
RC TISSUE=platelet;
RX MEDLINE=98113162; PubMed=9442040;
RA Jin J., Daniel J.L., Kunapuli S.P.;
RT "Molecular basis for ADP-induced platelet activation. II. The P2Y1
RT receptor mediates ADP-induced intracellular calcium mobilization and
RT shape change in platelets.";
RL J. Biol. Chem. 273:2030-2034(1998).
CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC ATP AND ADP. IN PLATELETS BINDING TO ADP LEADS TO MOBILIZATION OF
CC INTRACELLULAR CALCIUM IONS VIA ACTIVATION OF PHOSPHOLIPASE C, A
CC CHANGE IN PLATELET SHAPE, AND PROBABLY TO PLATELET AGGREGATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- INDUCTION: REPRESSED BY THE P2Y1 RECEPTOR-SPECIFIC ANTAGONISTS
CC A3P5P, A3P5P AND A2P5P. THESE INHIBIT CALCIUM ION MOBILIZATION
CC AND SHAPE CHANGE IN PLATELETS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: Z49205; CAA89066.1; -
DR EMBL: U42030; AAA97873.1; -
DR EMBL: U42029; AAA97872.1; -
DR EMBL: S81950; AAB47091.1; -
DR EMBL: AJ006945; CAA07339.1; -
DR EMBL: AF018284; AAB94556.1; -
DR HSSP: P34996; 1DDO.
DR Genew; HGNC:8539; P2RY1.
DR MIM: 601167; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECPR_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECPR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Platelet;
KW Blood coagulation.
FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 53 74 1 (POTENTIAL).
FT DOMAIN 75 87 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 127 147 3 (POTENTIAL).
FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 167 188 4 (POTENTIAL).
FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 266 285 6 (POTENTIAL).
FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 304 328 7 (POTENTIAL).
FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 138 138 MISSING (IN REF. 1).

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SQ SEQUENCE 373 AA; 42071 MW; 4DC7C68BB4145392 CRC64;
Query Match 32.0%; Score 567; DB 1; Length 373;
Best Local Similarity 36.1% Pred. No. 2.le-30;
Matches 108; Conservative 68; Mismatches 119; Indels 4; Gaps 2;

OY CTDENIPFLKMHVIVIGIIFVLGFPPGNNAVISTYIKMPKPKSKSTIIIMLACTDLYL 83
   | : ||| ::||::||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db 42 CALTKTFQFORYITPAVVIILFFIICGLNSVAIMEFYHMKPWSISITYRMFLADLVY 101

OY 84 TSLPELIHYASGEMNIFGDPMCKFIKRFSPHFNLYSILFELTCFSIFRYCIHHMPCFS 143
   ||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db 102 LTPALIFYEYNFKTDWIFGDAMCKLRPFHVNLGYSGILEFTCSIRARSGVVPLKSLG 161

OY 144 IHKRCAVACAAVWIISIYAIVFMFLINSTNTNS-ACLDTSSDELNTIKWYLIL 202
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
   b 162 RLKKNMKICISVLMLVVAISPILFEYSGVGKNRRTICYDDTSDSELSAFYISMCT 221

OY 203 TATFECPLIVLTLCYTTHITHTLHRGHGTDSCLKOKARRTLITLLAFVYCFLPHILRV 262
   ||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db 222 TVAEFCVPVILIAGCYGLIAYALYKDLDNSPLRKSIYLTVIITYFAVSYPEFHMT 281

OY 263 IRIESRL---LSICSIEINOIHENAIYISRPLAINTFNILLIYVSDNFQAQVCSTR 318
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
   Db 282 MLNEARILDFOPTAPCAFNDRVYATYQVTBGLIASINSCVDPILEYLAGTEFRRLRSRAVR 340

RESULT 3
P2YR.CHICK STANDARD; PRT; 362 AA.
AC P34996;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE P2Y purinoceptor 1 (ATP receptor) (p2y1) (purinergic receptor).
GN P2RX1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-Brain;
RC MEDLINE=93285340; PubMed=8508924;
RA Webb T.E., Simon J.J., Krishnek B.J., Bateson A.N., Smart T.G.,
RA Kling B.F., Burnstock G., Barnard E.A.;
RT "Cloning and functional expression of a brain G-protein-coupled ATP
RT receptor."
RL FEBS Lett. 324:219-225(1993).
RN [2]
RN 3D-STRUCTURE MODELING.
RP MEDLINE=97026278; PubMed=8872457;
RX van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;
RT Drug Des. Discov. 13:133-140(1995).
RL "Modelling the p2y purinoceptor using rhodopsin as template.";
CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN
CC INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GO FAMILY THAT
CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN. SPINAL CORD. GASTROINTESTINAL TRACT,
CC SPLEEN AND LEG MUSCLE. IS NOT DETECTED IN THE HEART, LIVER,
CC STOMACH, LUNG AND KIDNEY.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR	EMBL: X73268; CAA51716.1; .
DR	PIR: S33733; S33733.
DR	PDB: 1DDJ; 1I-JUL-96.
DR	InterPro: IPR000276; GPCR_Rhodopsn.
DR	Pfam: PF00001; 7tm_1; 1.
DR	PRINTS: PR00237; GPCRRHODOPSN.
DR	PROSITE: PS00237; G_PROTEIN_RECPT_FL_2; 1.
DR	PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; 3D-structure.
FT	DOMAIN 1
FT	TRANSMEM 42 63
FT	DOMAIN 64 76
FT	TRANSSEM 67 98
FT	DOMAIN 99 115
FT	TRANSSEM 116 136
FT	DOMAIN 137 155
FT	TRANSSEM 156 177
FT	DOMAIN 178 207
FT	TRANSSEM 208 227
FT	DOMAIN 228 254
FT	TRANSSEM 255 274
FT	DOMAIN 275 292
FT	TRANSSEM 293 317
FT	DOMAIN 318 362
FT	DISULFD 113 191
FT	CARBOHYD 11 26
FT	CARBOHYD 26 102
FT	CARBOHYD 102 186
FT	CARBOHYD 186 362 AA;
SO	SEQUENCE
Query Match	31.9%; Score 565.5; DB 1; Length 362;
Best local similarity	35.0%; Pred. No. 2,5e-30;
Matches 115;	Conservative 66; Mismatches 137; Indels 11; Gaps 4;
OY	1 MNEPLDIYANASDEPDVYA---AFGNS---CTDENIPILKMHLYPVITYGIIIFLVEPPGNAY 53
Db	1 MTEALISALMGCTOPELLAGGMAAMNATTKCSLTGTGGFOFYLLPVTYIVLVFTTGLFGNSV 60
OY	54 VISTYTFEMRPWKSKSTFIMLNACDIDLINSPLPHIVYASGEWMIFGDGCKFRFSF 113
Db	61 AIAHWVFEMRPMSGISTVMENIALADELYVLTPALPIIFYEKKTMIFEDVCKLQRFLE 120
OY	114 HFNLYSLFLTCESIFRYCYAIIHPMSEFSIHKTCAVAVACAVNIISLVAVIPMTFL- 172
Db	121 HNVIYGSILFLTCISVHRHTGVAPHLKSIGRLKKKNVAVSSVALVAVIAPLIFFYSG 180
OY	173 TSTNTNSACLDLSSDELNTIKMYNLILAFTFCCLPLYVITGLTYTHIHTHGLOTD 232
Db	181 TGVRNRKTTICDTTADELKRSYFYSMTTVFMCKIPETIVLGSETGLVKALITYKDLDN 240
OY	233 SCILQKARRLITLLLAIFYCVCFPHILIRVIRIESRL---LSISCSIENNHEAVIVSRP 289
Db	241 SPLRKRSIYIVIVLVFAVSYLPHPMKTLMLRARLDQFPQMCAFNDKVAYATGYOVTRG 300
OY	290 LAALTFGNLLIYVVSDNFQAQVCSTYR 318
Db	301 LASINSCVDPIIYFLAGDTFRRRIISRATR 329
RESULT 4	
ID	P2YR_MELGA STANDARD; PRT; 362 AA.
AC	P49652;
DT	01-FEB-1996 (Rel. 33, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	15-JUL-1998 (Rel. 36, Last annotation update)
DE	P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor) (6HI orphan receptor).
GN	P2R1.
OS	Melanagris gallopavo (Common turkey).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Archaeosuria; Aves: Neognathae; Galliformes; Meleagrididae; Meleagris.
XX NCBI_TaxId=9103;
RN [1]
RC SEQUENCE FROM N.A.
RP TISSUE=Brain;
RA MEDLINE=94335907; PubMed=8058061;
RX Filiz T.M., Li O., Boyer J.L., Nicholas R.A., Harden T.K.;
RT "Expression of a cloned P2Y purinergic receptor that couples to
RL phospholipase C.";
RM Mol. Pharmacol. 46:8-14(1994).
RN [2]
RX SEQUENCE FROM N.A.
RA MEDLINE=97382456; PubMed=9240460;
RX Li O., Schachter J.B., Harden T.K., Nicholas R.A.;
RT "The 6k1 orphan receptor, claimed to be the p2y5 receptor, does not
RL mediate nucleotide-promoted second messenger responses.";
CC Blochem. Biophys. Res. Commun. 236:455-460(1997).
CC -1 FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN
CC INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GO FAMILY THAT
CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC -1 SUBCELLULAR LOCATION: Integral membrane protein.
CC -1 TISSUE SPECIFICITY: MAINLY FOUND IN BLOOD, BRAIN, AND LUNG. TO A
CC LESSER EXTENT IN STOMACH, GUT, AND SKELETAL MUSCLE.
CC -1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC CC
DR EMBL: U09842; AAA18784.1; .
DR DR
DR HSSP: AF012103; AAB65428.1; .
DR DR
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1.1.
DR PRINTS: PR00237; GPCRRHODPSN.
DR PROSITE: PS00237; G-PROTEIN_REC_P1.1; 1.
DR PROSITE: PS02622; G-PROTEIN_REC_P1.2; 1.
KW G-Protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 41
FT TRANSMM 42 63
FT FT 64 76
FT DOMAIN 64 76
FT TRANSMM 77 98
FT FT 99 115
FT DOMAIN 116 136
FT TRANSMM 137 155
FT FT 156 177
FT TRANSMM 178 207
FT DOMAIN 208 227
FT TRANSMM 228 254
FT FT 255 274
FT TRANSMM 275 292
FT DOMAIN 293 317
FT TRANSMM 318 362
FT FT 362 373
FT DISULFID 113 191
FT CARBOHYD 11 11
FT CARBOHYD 26 26
FT CARBOHYD 102 102
FT CARBOHYD 186 186
SQ SEQUENCE 362 AA; 41180 MW; 3E128AB9EB64349C CRC64;

Query Match 31.9%; Score 565.5; DB 1; Length 362;
Best Local Similarity 35.0%; Pred. No. 2.5e-30;
Matches 115; Conservative 66; Mismatches 137; Indels 11; Gaps 4;

1 MNEDPLDIANASDEPDYAA---AFGN-----CTDENIPFLKMHYLVVIGIPLVGFPNNAV 53
| | | | | : | | | | | : ||| : ::|| : ||||
1 MTEALLISALANGTPPELLAGWGMAAGNSSTCKSLTKTGQFOFYLLPTVTYIIIVFITGLGNSV 60

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ID	P2YR_RAT	STANDARD:	PRT:	373 AA.
AC	01-FEB-1996 (Rel. 33, Created)			
AD	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-FEB-1996 (Rel. 33, Last annotation update)			
DE	P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).			
GN	P2RY1.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Insulinoma;			
RX	MEDLINE=95298025; PubMed=7779087;			
RA	Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;			
RT	"Cloning of rat and mouse P2Y purinoceptors."			
RL	Biochem. Biophys. Res. Commun. 211:211-218(1995).			
CC	-1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS			
CC	ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECTS			
CC	OF EXTRACELLULAR ATP ON INSULIN SECRETION.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN MUSCLE, HEART, LIVER, KIDNEY,			
CC	LUNG, BRAIN, SPLEEN, BUT NOT IN TESTIS.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	-----			
DR	EMBL; U22830; AAA91303.1; -			
DR	HSSP; P34996; IDDD.			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tmL1.1.			
DR	PRINTS; PR00237; GPCRHHODPSN.			
DR	PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.			
DR	PROSITE; PS0262; G-PROTEIN_RECP_F1_2; 1.			
KW	G-Protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1 52			
FT	TRANSMEM 53 74			
FT	TRANSMEM 75 87			
FT	DOMAIN 88 109			
FT	TRANSMEM 110 126			
FT	TRANSMEM 127 147			
FT	DOMAIN 148 166			
FT	TRANSMEM 167 188			
FT	TRANSMEM 188 188			


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FT DOMAIN 189 218 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 266 285 6 (POTENTIAL).
FT DOMAIN 286 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 328 7 (POTENTIAL).
FT DOMAIN 329 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42321 MW; 6DDF676287B5E648 CRC64;

Query Match 31.9%; Score 565; DB 1; Length 373;
Best Local Similarity 36.8%; Pred. No. 2,8e-30;
Matches 107; Conservative 67; Mismatches 113; Indels 4; Gaps 2;

QY 32 KMHLPIYGIIFLPGFPGNAVISTYIFKRPKSSITIMLNACTDLYLSLPLIH 91
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 50 QFYLPAYILVFIIFLGNSVALIMFVFMKPSGISVYFNLADELVLPLALIF 109
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 92 YVASEMWIFGDEPKFIRSFHNLVSYLFLCFISFYCVIHPMSGFSIHKTCAV 151
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 110 YFFKTDWIFGDMVKLQRFIFHNLVGSILFLCISAHRSVGVYPLKSLGRKKNAI 169
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 152 VACAVWIIISLVAVIPMTFLTSNRTNRS-ACLDLTSDELNTIKYNLLTFTCLP 210
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 170 YVSVLWLVIVVAISPILFYSGTGIRKKVTCYDSDELRSFYISMCTVYAMFETIP 229
   :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 211 LVIVTLCYTTIHTLFGLOTDSCLOKARRLTILLAFVCEPFIHLVIRIESRL- 269
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 230 LVLLIGCGGLVRLALIKDLDNSLRKRSIYLVIVLVFAVSIPIFPMVTMNLRLD 289
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 270 --LSISCSIEHQIHEAVIVSRPLAALNTFENLLYVVVSDNFQOAVCSTVR 318
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 290 FQFPEMCDPNDRVATYATQVTRGLASLNSCVDPIILYFLAGDTFRRLSRATR 340
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 6
P2YR_BOVIN STANDARD; PRT; 373 AA.
AC P48042;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN P2RY1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Corpus callosum;
RX MEDLINE=99064562; PubMed=9848096;
RA Deng G., Matute C., Kumar C.K., Fogarty D.J., Miledi R.;
RT "Cloning and expression of a P2Y purinoceptor from the adult bovine
RL corpus callosum."
RT Biochem. Biophys. Res. Commun. 212:648-656(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Corpus callosum;
RX MEDLINE=99064562; PubMed=9848096;
RA Deng G., Matute C., Kumar C.K., Fogarty D.J., Miledi R.;
RT "Cloning and expression of a P2Y purinoceptor from the adult bovine
RL corpus callosum."
RT Neurobiol. Dis. 5:259-270(1998).
CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC ATP AND ADP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----

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CC -----
DR EMBL; X87628; CA60958.1; -
DR EMBL; U34041; AAC78275.1; -
DR HSSP; P34996; 1DD.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECPEP_F1.1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPEP_F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 53 74 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 75 87 2 (POTENTIAL).
FT TRANSMEM 88 109 2 (POTENTIAL).
FT DOMAIN 110 126 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 147 3 (POTENTIAL).
FT DOMAIN 148 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 188 4 (POTENTIAL).
FT DOMAIN 189 218 5 (POTENTIAL).
FT TRANSMEM 219 238 5 (POTENTIAL).
FT DOMAIN 239 265 6 (POTENTIAL).
FT TRANSMEM 266 285 7 (POTENTIAL).
FT DOMAIN 286 303 7 (POTENTIAL).
FT TRANSMEM 304 328 7 (POTENTIAL).
FT DISULFID 124 202 BY SIMILARITY.
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 27 27 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42287 MW; 9270A7175C0BDA76 CRC64;

Query Match 31.7%; Score 562; DB 1; Length 373;
Best Local Similarity 36.1%; Pred. No. 4,4e-30;
Matches 108; Conservative 67; Mismatches 120; Indels 4; Gaps 2;

QY 24 CTDENIPKMHVLPVYGIIFLPGFPGNAVISTYIFKRPKSSITIMLNACDLYL 83
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 42 CALTKTGQFYLPVAVILVFIIFLGNSVALIMFVFMKPSGISVYFNLADELVL 101
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 84 TSLPFLHYVASEMWIFGDEPKFIRSFHNLVSYLFLCFISFYCVIHPMSGFS 143
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 102 LTLPLALIVYFNKTDWIFGDMVKLQRFIFHNLVGSILFLCISAHRSVGVYPLKSLG 161
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 144 IHKTRCAVACAVWIIISLVAVIPMTFLTSNRTNRS-ACLDLTSDELNTIKYNIL 202
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 162 RLKRNNAVYISVLWLVVGVISPLFYSGTGIRKKVTCYDSDELRSFYISMCT 221
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 203 TATFPCLPVIVTLCYTTIHTLFGLOTDSCLOKARRLTILLAFVCEPFIHLVIR 262
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 222 TVAMFCVPLVILGCTGILVRLALIKDLDNSLRKRSIYLVIVLVFAVSIPIFPM 281
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 263 IRISSRL--LSISCSIEHQIHEAVIVSRPLAALNTFENLLYVVVSDNFQOAV 318
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 282 MNLRLDFOFPEMCAFNDRVATYATQVTRGLASLNSCVDPIILYFLAGDTFRRL 340
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 7
P2Y8_XENLA STANDARD; PRT; 537 AA.
AC P79928;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE P2Y purinoceptor 8 (P2Y8).
GN P2RY8.

```

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 CC NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Neural plate;
 RA MEDLINE=97284734; PubMed=9139711;
 RX Bogdanov Y.D., Dale L., King B.F., Whitlock N., Burnstock G.;
 RT "Early expression of a novel nucleotide receptor in the neural plate
 of Xenopus embryos.";
 RL J. Biol. Chem. 272:12583-12590(1997).
 CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ATP, UTP, GTP AND ITP.
 CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
 CC ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC MAY PLAY A KEY ROLE IN THE EARLY DEVELOPMENT OF NEURAL TISSUE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: X99593; CAA68213.1; -
 DR HSSP: P34996; IDDD
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G-PROTEIN RECP FL 1; 1.
 DR PROSITE: PS50262; G-PROTEIN RECP FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 49
 FT TRANSSEM 50 70
 FT TRANSSEM 71 79
 FT TRANSSEM 80 100
 FT TRANSSEM 101 118
 FT TRANSSEM 119 139
 FT TRANSSEM 140 161
 FT TRANSSEM 162 182
 FT TRANSSEM 183 210
 FT TRANSSEM 211 231
 FT TRANSSEM 232 254
 FT TRANSSEM 255 275
 FT DOMAIN 276 292
 FT TRANSSEM 293 316
 FT DOMAIN 317 537
 FT DISULFID 116 193
 FT CARBOHYD 26 29
 FT CARBOHYD 29 29 N-LINKED (GLCNAC...) (POTENTIAL).
 SEQUENCE 537 AA; 62024 MW; BZCF24812F3C19F2 CMC64;
 Query Match 31.58; Score 557; DB 1; Length 537;
 Best Local Similarity 34.28; Pred. No. 1.3e-29;
 Matches 116; Conservative 70; Mismatches 139; Indels 14; Gaps 4;
 DB 20 PKMLKMLTNDTDEICVF---DEG--FKPELLFVSVAFFMGLPNTIAMMFIKMR 73
 QY 4 PLDYLANASDPDDAAAFNGCTDENIPLKMHYLPVYIGIIFLVGPPGNAVVISIYIKMR 63
 DB 64 PKMSSTIMLNACTDLYLTLSPFLHYHVAAGENGDFGDMCFIFESFHNLSYSLF 123
 DB 74 PAMPTIYVMMNLASDLVLYSLPTLYVYADKNNMFGVYCKLVFLFYANLYSSILF 133
 QY 124 LFGFSIFRYCVIIHPMSCFSIHKTRCAVAVCAVMMIISLAVVIMPLFITSTNNTNSAC 183
 DB 134 LFGISVRYRGVCHPITSRLRMAKHAIVYICALVWLSVTLCIYVNLFLFVSPVKVNTIC 193
 QY 184 LDIATSSDELNTIKMYNLIATATTCFLPLVIVTLCYTTIHTLHGL-----QTDSCIKOK 238

DB 194 HDTTRPEDFARVVESTAIMCLLFGIIPDLIIAGCGIMTRRELMPYVSGNOCTPYSYKRR 253
 QY 239 ARRLIILLLFYVCELFPHILRYIRISRLISCSLENOIHEAYIYSRPLAALNTFNG 298
 DB 254 SIKTIIFWIAFCEIMPHETRLTYRYARLGLICVLANVINTYKTRPLASNSCID 313
 QY 299 LLLVYVSDNFQOAVCTVRCKVSGNLEQARKISYNNP 337
 DB 314 PLVFLANDRRRLRIIRIVRRSS---VPRNRMHTNHP 349
 RESULT 8
 P2Y4_HUMAN
 ID P2Y4_HUMAN STANDARD: PRT; 365 AA.
 AC P51582;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 4 (P2Y4) (Uridine nucleotide receptor) (UNR) (P2P).
 GN P2RY4 OR NRU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96125055; PubMed=8537336;
 RA Communi D., Piroton S., Parmentier M., Boeynaems J.-M.;
 RT "Cloning and functional expression of a human uridine nucleotide
 RT receptor.";
 RL J. Biol. Chem. 270:30849-30852(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96125054; PubMed=8537335;
 RA Nguyen T., Erb L., Weisman G.A., Marchese A., Heng H.H.Q.,
 RA Garrard R.C., George S.R., Turner J.T., O'Dowd B.F.;
 RT "Cloning, expression, and chromosomal localization of the human
 RT uridine nucleotide receptor gene.";
 RL J. Biol. Chem. 270:30845-30848(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Pancreas;
 RX MEDLINE=96197801; PubMed=8617367;
 RA Stam N.J., Kloppe J., van der Heuvel M., Olijve W.;
 RT "Molecular cloning and characterization of a novel orphan receptor
 RT (P2P) expressed in human pancreas that shows high structural homology
 RT to the P2U purinoceptor.";
 RL FEBS Lett. 384:260-264(1996).
 CC -1- FUNCTION: Receptor for UTP and UDP coupled to G-proteins that
 CC activate a phosphatidylinositol-calcium second messenger system.
 CC Not activated by ATP or ADP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Pancreas.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X91852; CAA62963.1; -
 DR EMBL: U40223; AAC50347.1; -
 DR EMBL: X96597; CAA65415.1; -
 DR HSSP: P34996; IDDD.
 DR Genew: HGNC:8542; P2RY4.
 DR MIM: 300038; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.

DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Polymorphism.
 FT DOMAIN 1 34
 FT TRANSMEM 35 61
 FT DOMAIN 62 72
 FT TRANSMEM 73 95
 FT DOMAIN 96 112
 FT TRANSMEM 113 131
 FT DOMAIN 132 151
 FT TRANSMEM 155 174
 FT DOMAIN 175 196
 FT TRANSMEM 197 222
 FT DOMAIN 223 246
 FT TRANSMEM 247 269
 FT DOMAIN 270 287
 FT TRANSMEM 288 309
 FT DOMAIN 310 365
 FT DISULFID 108 185
 FT VARIANT 168 168
 FT VARIANT 178 178
 FT VARIANT 191 191
 FT CONFLICT 86 86
 FT CONFLICT 234 234
 SQ SEQUENCE 365 AA; 40963 MW; 23E0AFED3B7BDEED CRC64;

Query Match 29.0%; Score 514; DB 1; Length 365;
 Best Local Similarity 35.1%; Pred. No. 5.7e-27;
 Matches 101; Conservative 64; Mismatches 119; Indels 4; Gaps 2;

QY 26 DENILKMHVPIVIGIIFLPGFNNAVISTYIFKMRPMKSTIIMNLACTDLIXLTS 85
 DB 30 DED--FKTILFVSTAVFVLGLNAPLTLFIRLRWDATFATYMEFLASDLYLVS 87
 QY 86 LPFLHYASGEMTFGDMCKFRFSEFHNLYSILFLTCISIFRYCVIHHMCSFSIH 145
 DB 88 LPTLYYAAAHNMFPGTEICKFVFLFWMNLKCVLFLTCISVHRIGICHPRLRLRG 147
 QY 146 KTRCAVACAVVWIIISLVAVIMPLITSTNRTNSACIDLTSDELNTIKWNLITAT 205
 DB 148 RPLRLAGLCLAVLWVAGCLVPLNLFVVTSTNKGTYLCHDTRPEFDHYVHSSAVML 207
 QY 206 TFCLELVITLCTYTIHITLHGL--QIDSCAKQARRTITILLAFYCGFLPHILAVI 263
 DB 208 LFGVCLVTVLCYGLMARLQPLPGSSASSRSLSLRTIAVLLVFAVCVFPFHITRTI 267
 QY 264 RIESRLSISCSIEQIHNAVIVSRPLALNFGNLLVYVSDNQ 311
 DB 268 YLARLLEADCRVLNIVNVVYKTRPLASNSCLDPVLYLLGDKYR 315

RESULT 9
 P2Y4_RAT
 ID P2Y4_RAT STANDARD: PRT; 361 AA.
 AC 035811:
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 4 (P2Y4).
 GN P2Y4 OR P2Y4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Liver;
 RA Bogdanov Y.D., Wildman S., King B.F., Burntack G.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Brain;
 RX MEDLINE=98421785; PubMed=9751165;
 RA Webb T.E., Henderson D., Roberts J.A., Barnard E.A.;
 RL "Molecular cloning and characterization of the rat P2Y4 receptor."
 J. Neurochem. 71:1424-1434(1998).
 CC -1- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
 activate a phosphatidylinositol-calcium second messenger system.
 CC Not activated by ADP or UDP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed at low levels. In brain,
 CC higher expression in the pineal gland and ventricular system.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: Y14705; CAA75007.1; -
 DR EMBL: Y11433; CAA72241.1; -
 DR HSSP: P34996; 1DD.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PR00001; 7tm1.1; -
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 30
 FT TRANSMEM 31 58
 FT DOMAIN 59 68
 FT TRANSMEM 69 91
 FT DOMAIN 92 108
 FT TRANSMEM 109 127
 FT DOMAIN 128 149
 FT TRANSMEM 150 170
 FT DOMAIN 171 192
 FT TRANSMEM 193 218
 FT DOMAIN 219 242
 FT TRANSMEM 243 265
 FT DOMAIN 266 283
 FT TRANSMEM 284 305
 FT DOMAIN 306 361
 FT DISULFID 104 181
 FT CARDHYD 175 175
 SQ SEQUENCE 361 AA; 40893 MW; 0377F96E5B449A3 CRC64;

Query Match 28.9%; Score 512; DB 1; Length 361;
 Best Local Similarity 34.2%; Pred. No. 7.6e-27;
 Matches 105; Conservative 66; Mismatches 126; Indels 10; Gaps 4;

QY 15 PYAAAFNCQDENIPLKMHVPIVIGIIFLPGFNNAVISTYIFKMRPMKSTIIMNL 74
 DB 14 PSPSGDGGCR-FNEFKTILPLMSYAVFVLGLNALNAPLTLFIRLRPMATATYMH 72
 QY 75 IACTDLVLTSLPLIHYASGEMTFGDMCKFRFSEFHNLYSILFLTCISIFRYCV 134
 DB 73 LALSPLTVLSPLTVYVYAAAHNMFPGTEICKFVFLFWMNLKCVLFLTCISVHRIG 132
 QY 135 IHHMCSFSIHKTRCAVACAVVWIIISLVAVIMPLITSTNRTNSACIDLTSDELNT 194
 DB 133 ICHPLRAIRWGRPRASLCLGAWLVVAGCLVPLNLFVVTNNGTTLCHDTPLEEDH 192
 QY 195 IKWNIILATFTFCPLVITLCTYTIHITLHGL----QIDSCAKQARRTITILLAF 250
 DB 193 YTFSSAVVLLFGLPFLITVLCYGLMARLRLPLPGAGSSRL--SLRTIAVYLVIF 250
 QY 251 YVCELPFHILVIRIESRLSISCSIEQIHNAVIVSRPLALNFGNLLVYVSDNQ 310
 DB 251 AVCFVFPFHITRTIYQARLLQADCRVLNIVNVVYKTRPLASNSCLDPVLYLLGDKYR 310

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OY      311  ---OAVC 314
Db      311  NOLQOQC 317

RESULT 10
P2Y4_MOUSE
ID      P2Y4_MOUSE      STANDARD:      PRI:      361 AA.
AC      Q9JUS7,
DT      15-JUN-2002 (Rel. 41, Created)
DT      15-JUN-2002 (Rel. 41, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      P2Y4 purinoceptor 4 (P2Y4).
NM      P2RY4 OR P2Y4R.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      NCBI_TaxID=10090;
RP      [1]
RQ      SEQUENCE FROM N.A.
RC      STRAIN=129/SvT;
RX      MEDLINE=21185993; PubMed=11290369;
RA      Suarez-Huerta N., Pouillon V., Boeynaems J.-M., Robaye B.;
RT      "Molecular cloning and characterization of the mouse P2Y4 nucleotide
RT      receptor";
RL      Eur. J. Pharmacol. 416:197-202(2001).
CC      -1- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
CC      activate a phosphatidylinositol-calcium second messenger system.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- TISSUE SPECIFICITY: Expressed in the liver, intestine, stomach,
CC      bladder and lung.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
-----
CC      EMBL: AJ277752; CAB91043.1; -
DR      HSSP: P34996; IDDD.
DR      MGD: MGI:1926594; P2Y4.
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm_1.1.
DR      PRINTS: PR00237; GPCRHRDOPSN.
DR      PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR      PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein.
KW      DOMAIN
FT      TRANSSEM      1      30
FT      DOMAIN      1      58
FT      TRANSSEM      31      68
FT      DOMAIN      59      68
FT      TRANSSEM      69      91
FT      DOMAIN      92      108
FT      TRANSSEM      109      127
FT      DOMAIN      128      149
FT      TRANSSEM      150      170
FT      DOMAIN      171      192
FT      TRANSSEM      193      218
FT      DOMAIN      219      242
FT      TRANSSEM      243      265
FT      DOMAIN      266      283
FT      TRANSSEM      284      305
FT      DOMAIN      306      361
FT      DISULFID      104      181
FT      CARBOHYD      175      175
SQ      SEQUENCE      361 AA; 41034 MW; 3E8EA84B5BC0A20 CRC64;

Query Match      28.4%: Score 503; DR 1; Length 361;
Best Local Similarity      33.9%: Pred. No. 2.9e-26;
Matches      107; Conservative      65; Mismatches      134; Indels      10; Gaps      4;

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Qy	6	DYLANASOPEPYAAFGCQDTEENPLKMHNYLPVYUGJILFLVGFPGNNAVISTYLEFKRPM	65
Db	5	DSLFLSTLIGBSPSSGDDGC-KFNEEFKFLIPDLSYAVAFVGLALMNPATLMFLFRLRPW	63
Qy	66	KSSPTIMLNINACTDLYLTLSLPHFIHYVYASGEMNI FGD FCKEITRFSEHNLVSSILFLT	125
Db	64	DATATYMFHALDSTLVLSLPLVLYYYAANNNHNPFGGCKFVRLFLYWNLYCSVLELT	123
Qy	126	CFSTFRVCVLIHPMSCSIRKTRCAVAVACAAVWIIISLVAYIPLMFLITSTIRKTRSCLD	185
Db	124	CISYHARWGCIOHPLRAIRWGRBPRFAGLIGLWLVAGCLVPLNLFVYTANNGTIIICHD	183
Qy	186	LTSDEINTKIMKYLLILATATFCPLIVYIVLTCTYTIHTLTHGL-----QDSCCKORAR	241
Db	184	TTLPEEDHYHYFSESTIMVLFGPELLITVYCYGLMARRLRPLPGAGQSSRL--RSLR	241
Qy	242	LTLILLATFYVCFPLPHILRYIRIESRLSISCSIEINOIHNAVIVSAPLALNTFGNILL	301
Db	242	TIAYVLVAFCVPEFHITRTIYTLARLNAECRVLIIVNVVYKVTBPLASANCIDPVL	301
Qy	302	YVYVSDNFQ--QAVC 314	
Db	302	YLFTGDKYRNOLQQLC 317	
RESULT 11			
ID	P2Y3-CHICK	STANDARD;	PRT; 328 AA.
AC	Q98907;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DE	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).		
GN	P2RY3.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=96319774; PubMed=8700132;		
RA	Webb T.E., Henderson D., King B.F., Wang S., Simon J.,		
RA	Bateson A.N., Burnstock G., Barnard E.A.;		
RT	"A novel G protein-coupled P2 purinoceptor (P2Y3) activated		
RL	preferentially by nucleoside diphosphates.";		
CC	Mol. Pharmacol. 50:258-265(1996).		
CC	-1- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADP > UTP > ATP = UDP. THE		
CC	ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE		
CC	A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
CC	CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	use by non-profit institutions as long as its content is in no way		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; X98283; CAA66930.1; -.		
DR	HSSP; P34996; IDDD.		
DR	InterPro; IPR000276; GPCR_Rhodopsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCRHDOPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; FALSE_NEG.		
DR	PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.		
FT	DOMAIN 1 22	EXTRACELLULAR (POTENTIAL).	
FT	TRANSNM 23 43	1 (POTENTIAL).	

```

RA  Im D.-S., Strocio R., Bellefleur J.N., Abramovitz M., Chang R.,
RA  Williams D.L. Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,
RA  Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
RA  Lynch K.R., Evans J.F.,
RA  "Characterization of the human cysteinyl leukotriene 2 receptor.";
RA  J. Biol. Chem. 275:30531-30536(2000).
RL  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE-20545741; PubMed-11093801;
RA  Natchaker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
RA  Cjvellil O.,
RT  "Molecular cloning and characterization of a second human cysteinyl
RT  leukotriene receptor: discovery of a subtype selective agonist.";
RL  Mol. Pharmacol. 58:1601-1608(2000).
RL  [4]
RP  SEQUENCE FROM N.A.
RA  Dunn M.;
RP  Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN  [5]
RA  Suga H.;
RP  SEQUENCE OF 17-346 FROM N.A.
RT  "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";
RT  Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC  mediated via a G-protein that activates a phosphatidylinositol-
CC  calcium second messenger system. Stimulation by BAY u9773, a
CC  partial agonist, induces specific contractions of pulmonary veins
CC  and might also have an indirect role in the relaxation of the
CC  pulmonary vascular endothelium. The rank order of affinities for
CC  the leukotrienes is LTC4 > LTD4 >> LTE4.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
CC  heart, placenta, spleen, peripheral blood leukocytes and adrenal
CC  gland. In lung, expressed in the interstitial macrophages, and
CC  slightly in smooth muscle cells.
CC  -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC  -----
CC  CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  DR  EMBL: AB038269; BAB03601.1; -.
DR  EMBL: AF254664; AAG17281.1; -.
DR  EMBL: AF279611; AAK69485.1; -.
DR  EMBL: AL137118; CAC29102.1; -.
DR  EMBL: AB041644; BAB16379.1; -.
DR  MIM: 605666; -.
DR  InterPro: IPR004071; Cysleuk_receptor.
DR  InterPro: IPR000276; GPCR_Rhodpsn.
DR  Pfam: PFO00001; 7tm.1; 1.
DR  PRINTS: PRO1533; CYSLTRREPTR.
DR  PRINTS: PRO0237; GPCR_RHODPSN.
DR  PROSITE: PS00237; G-PROTEIN_RECE_F1_1; FALSE_NEG.
DR  PROSITE: PS50262; G-PROTEIN_RECE_F2_1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein.
FT  DOMAIN 1 42
FT  TRANSSEM 43 63
FT  DOMAIN 64 72
FT  TRANSSEM 73 93
FT  DOMAIN 94 123
FT  TRANSSEM 124 144
FT  DOMAIN 145 153
FT  TRANSSEM 154 174
FT  DOMAIN 175 204
FT  TRANSSEM 205 225
FT  DOMAIN 226 245
FT  TRANSSEM 246 266
FT  DOMAIN 267 286
FT  TRANSSEM 287 307
FT  TRANSSEM 287 307

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FT DOMAIN 308 346 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 111 187 BY SIMILARITY.
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 346 AA; 39635 MW; EB54A4A2DCE5ED CRC64;
 Query Match 27.5%; Score 487.5; DB 1; Length 346;
 Best Local Similarity 34.9%; Pred. No. 2.9e-25;
 Matches 111; Conservative 64; Mismatches 114; Indels 29; Gaps 10;
 QY 23 NCIDENIPKMHYIPVYIGIIFLVGPGNAVITYIFKRPKMSST---IIMNLACTD 79
 DB 30 NCTIEN--FKREFPIYLIIFGVLGNG--LSIYVF--LQPKKSTSVNFMNLAIISD 84
 QY 80 LLYTSLPFLIHYAAGENNIFGDMCKFRFSFHPNYSILITGCSIFRCVITHPM 139
 DB 85 LRFISTLPFRADYILKRSNWFGLDACLKIMSYSLVNMYSIYFLVLSVFRFLAMWPF 144
 QY 140 SCESIHTRCAVAVACAVVMIISLVAVIPMFELITSTNTRNSACLDITSSDELNTIK-- 196
 DB 145 RLHVTISRSAMWICGIMILIMAST---MLDSSGSDNGS---VTSCELMNLKTKAK 197
 QY 197 --WNLULATFPCPLVYIVTLCYTTIIHITLHGLQDSCK---QKARLITILLAFY 251
 DB 198 LQTNMYIALVVGCLPFETLSICLLIIRYLKAVESEGSLRVSHRRALTTIITLIIF 257
 QY 252 VCFPLPHILRYIRIESRLTISCSIEENOIHEAVYSPRIALNFGNLLYVVSNDNQ 311
 DB 258 LCFPIYTLRLVHLTKTKVGL---CKDLKHALVITLALAAANCFNLLTYFAGEENKD 314
 QY 312 AVCSVTRCKVSGNLEQAK 329
 DB 315 RLKSLR---KGHPQAK 329
 Db
 RESULT 13
 P2Y2_MELGA STANDARD; PRT; 328 AA.
 ID P2Y2_MELGA
 AC O93361;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
 GN P2RY3.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OX NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98401046; PubMed=9730913;
 RA Li O., Olesky M., Palmer R.K., Harden T.K., Nicholas R.A.:
 RT "Evidence that the p2y3 receptor is the avian homologue of the
 RL mammalian p2y6 receptor."
 CC Mol. Pharmacol. 54:541-546(1998).
 CC -1- FUNCTION: RECEPTOR FOR EXTRACELLULAR UDP< ADP - UTP. THE ACTIVITY
 CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
 CC PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: AF069555; AAC23863.1;
 DR HSSP; P34996; IJDD.

DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN_RECPT_FL1; FALSE_NEG.
 DR PROSITE; PS50262; G-PROTEIN_RECPT_FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 22
 FT TRANSMEM 23 43
 FT DOMAIN 44 57
 FT TRANSMEM 58 78
 FT DOMAIN 79 96
 FT TRANSMEM 97 117
 FT DOMAIN 118 139
 FT TRANSMEM 140 160
 FT DOMAIN 161 189
 FT TRANSMEM 190 210
 FT DOMAIN 211 231
 FT TRANSMEM 232 252
 FT DOMAIN 253 275
 FT TRANSMEM 276 298
 FT DOMAIN 299 323
 FT CARBOHYD 5 5
 FT DISULFID 94 172
 SQ SEQUENCE 328 AA; 37594 MW; B74D9B99C7164A5 CRC64;
 Query Match 27.5%; Score 486.5; DB 1; Length 328;
 Best Local Similarity 35.9%; Pred. No. 3.2e-25;
 Matches 111; Conservative 55; Mismatches 124; Indels 19; Gaps 8;
 QY 16 DYAAFGNCIDENIPKMHYIPVYIGIIFLVGPGNAVITYIFKRPKMSSTIIMNL 75
 DB 5 NCTIEN--FKREFPIYLIIFGVLGNG--LSIYVF--LQPKKSTSVNFMNLAIISD 84
 QY 76 ACTDLVLTSLPFLIHYAAGENNIFGDMCKFRFSFHPNYSILITGCSIFRCVY 135
 DB 64 ATADLVYCSPLIYNTQDWPFGFTCKFYRFQYTNLHGSILITGCSIFRCVY 123
 QY 136 IHPMCSFIRK---TRCAVAVACAVVMIISLVAVIPMFELITST--NRNRSACLDITSD 191
 DB 124 CHPLA--SMHKKKKKLTWICCAVWFIACPL--TFEVSSTGTORNRVTCYDLSPPDR 180
 QY 192 LNTIKWNLITATFPCPLVYIVTLCYTTIIHITLHGLQDSCK-----KOKARLTI 244
 DB 181 SASYPPYIGITLTGFLPFAILLACYSMARIL---CQDELGLAVHKKKDAVAVMTI 237
 QY 245 LLLAFYVCFPLPHILRYIRIESRL--SISCSIEENOIHEAVYSPRIALNFGNLLYV 303
 DB 238 IVTVVFSFPHILTYIVLVSSPTLPQTAALAVKCTRPFRASMSVADPILFY 297
 QY 304 VVSDNFOQA 312
 DB 298 FTQRRFRES 306
 Db
 RESULT 14
 P2Y2_RAT STANDARD; PRT; 374 AA.
 ID P2Y2_RAT
 AC P41232;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)
 GN Purinergic receptor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95110548; PubMed=7811468;
 RA Rice W.R., Burton F.M., Fiedelney D.T.:
 RT "Cloning and expression of the alveolar type II cell P2u-purinergic

```

RT receptor ;
RL Am. J. Respir. Cell Mol. Biol. 12:27-32(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Wistar; TISSUE-Pituitary;
RA Chen Z.P., Krull N., Xu S., Levy A., Lightman S.L.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Wistar;
RA MEDLINE=98099857; Pubmed=9437211;
RA Seye C.I., Gadeau A.P., Daret D., Dupuch F., Alzieu P., Capron L.,
RA Desgranges C.;
RT "Overexpression of P2Y2 purinoceptor in intimal lesions of the rat
aorta.
RL Arterioscler. Thromb. Vasc. Biol. 17:3602-3610(1997).
CC -1- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
CC activate a phosphatidylinositol-calcium second messenger system.
CC The affinity range is UTP - ATP > ATP-gamma-S >> 2-methylthio-ATP
CC = ADP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; D09402; AAA61565.1; -
DR EMBL; L46865; AAB0209.1; -
DR EMBL; U56839; AAC00048.1; -
DR HSSP; P34996; 1DDP.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN_RECPT_P1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECPT_P2_1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSMM 33 59
FT TRANSMM 60 70
FT DOMAIN 71 93
FT TRANSMM 94 110
FT TRANSMM 111 129
FT DOMAIN 130 152
FT TRANSMM 153 172
FT TRANSMM 173 194
FT TRANSMM 195 220
FT DOMAIN 221 245
FT TRANSMM 246 268
FT TRANSMM 269 287
FT DOMAIN 287 308
FT TRANSMM 309 374
FT CARBOHD 9
FT CARBOHD 13
FT DISULFD 106 183
FT CONFLCT 132 132
FT CONFLCT 132 132
FT CONFLCT 143 143
FT CONFLCT 146 166
FT CONFLCT 188 188
FT CONFLCT 188 188
SO SEQUENCE 374 AA; 42137 MW; 2DA653AA20A1AF3 CAC64;

Query Match 27.3%; Score 483.5; DB 1; Length 374;
Best Local Similarity 35.2%; Pred. 0.5; 5e-25;
Matches 99; Conservative 56; Mismatches 117; Indels 9; Gaps 2;

28 NIPLKMHRLPVTYIGILVPGPNAVYSTIIFKMRPKSKSTIMLNACDLDLYNSLP 87
28 NEDRRYVLLPVSIGYGVGLGLNVAALYIFLIRKKTNNASTYTFHFLAASDYSYASLP 87

```

Oy		86	FLHYHAASEBMTIFGDFMCKTFRSEGHNTKLSLITFLCEISFIPYVLIHPMSOFLHKT	147
Dd		88	LIVYYAAGDHMFSTVLCKLVRELFYNLYNCSILTEFLCISVHRCGLGVRLSHLSNGHA	147
Oy		148	RCAVWACAAVMIIISLVAVIPMPFLFTSTNRTRSACDLTSSDELNTIKWNLLPATEF	207
Dd		148	RVARRAAVVVVVVLVALACAPVLYEPTTYSRGTRICHTSARELFSHFVAVSMMGLLF	207
Oy		208	CLEPLVTLCVLTITTIHTL-----THGLOTDSCLQOKARLTIILLAFYVCFLPFHIR	261
Dd		208	AVPESLIIVCYVLMARLLKPAYGTGTLPR--AKRKSVRTALVLAVFALCFEPHVTR	264
Oy		262	VIRIESRLISTSCSIFENOHEMYIYSRPLAALNTFGNLLY	302
Dd		265	TLYSPRSIDLSCHTLNAINMAVKITRPASANSCLDEPLY	305
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RESULT 15				
P2Y2_MOUSE				
ID	P2Y2_MOUSE	STANDARD:	PRT;	373 AA.
AC	P35383; 009031; Q9CPZ4;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, last sequence update)			
DT	15-JUN-2002 (Rel. 41, last annotation update)			
DE	P21 purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)			
DE	(Purinerigic receptor).			
GN	P2RY2 OR P2RU1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NN	NCBI_TaxID=10090;			
NN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93281707; PubMed=7685114;			
RT	Lustig K.D., Shiau A.K., Brake A.J., Julius D.;			
RT	"Expression cloning of an ATP receptor from mouse neuroblastoma			
RT	cells";			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:5113-5117(1993).			
NN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96316177; PubMed=8793919;			
RT	Enomoto K., Furuya K., Moore R.C., Yamagishi S., Oka T., Maeno T.;			
RT	"Expression cloning and signal transduction pathway of P2U receptor			
RT	in mammary tumor cells";			
RL	Biol. Signals 5:9-21(1996).			
NN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SRRIN-C57BL/6J; TISSUE=Head, and Liver;			
RC	MEDLINE=21085650; PubMed=11217851;			
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Akaiwa T., Hara A., Fukunishi Y., Konno H., Aachi J., Fukuda S.,			
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schirral L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsi G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustinich S., Hill D., Hofman M., Hume D.A., Kamlya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
-RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
-RA	Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,			
RA	Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
NN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Breast tumor;			
RA	Straussberg R.;			

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP MUTAGENESIS OF LYS-107; ARG-110; HIS-262; ARG-265; LYS-289 AND
RX ARG-292.
RA MEDLINE-95181393; PubMed-7876172;
RA Erb L., Garrard R.C., Wang Y., Quinn T., Turner J.T., Weisman G.A.;
RT "Site-directed mutagenesis of P2U purinoreceptors. Positively charged
RT amino acids in transmembrane helices 6 and 7 affect agonist potency
RT and specificity.";
RL J. Biol. Chem. 270:4185-4188(1995).
CC -1- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
CC activate a phosphatidylinositol-calcium second messenger system.
CC The affinity range is UTP > ATP > ATP-gamma-S >> 2-methylthio-ATP
CC = ADP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: SPLEEN, TESTIS, KIDNEY, LIVER, LUNG, HEART AND
CC BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL; L14751; AAA39871.1; -;
DR EMBL; S83099; AAB50735.1; -;
DR EMBL; AK005013; BAB23746.1; -;
DR EMBL; AK017378; BAB30719.1; -;
DR EMBL; BC006613; AAH06613.1; -;
DR HSSP; P34996; 1DD.
DR MGD; MG1:105107; P2ry2.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN_RECIP_F1_1;
DR PROSITE; PS50262; G-PROTEIN_RECIP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSMEM 33 59
FT DOMAIN 60 70
FT TRANSMEM 71 93
FT DOMAIN 94 110
FT TRANSMEM 111 129
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FT DOMAIN 173 194
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SQ SEQUENCE 373 AA; 42174 MW; 590BBE502E41B3AE CRC64;
KDI -> PYV (IN REF. 2).
E -> D (IN REF. 2).
R -> L: DECREASE IN RECEPTOR ACTIVATION.
K -> I: NO EFFECT ON RECEPTOR ACTIVATION.
R -> L: DECREASE IN RECEPTOR ACTIVATION.
H -> L: DECREASE IN RECEPTOR ACTIVATION.
K -> I: NO EFFECT ON RECEPTOR ACTIVATION.
R -> L: DECREASE IN RECEPTOR ACTIVATION.
E -> D (IN REF. 2).
S -> R (IN REF. 2).
T -> N (IN REF. 2).
V -> M (IN REF. 2).
V -> L (IN REF. 3).
D -> N (IN REF. 2).
KDI -> PYV (IN REF. 2).

Query Match 27.0%; Score 479; DB 1; Length 373;
Best Local Similarity 34.4%; Pred. No. 1,1e-24;
Matches 97; Conservative 58; Mismatches 117; Indels 10; Gaps 2;
QY 28 NIPLKMYLPVYIGIIFLVGFGPGNAVISTYIFKRPKSSITIMLNACTDLYLSLP 87
DB 28 NEDFYVLLPVSYGVCVGLCLNVVALYIFLCRLKTNASTYWFHLAVSDSYAASLP 87
QY 88 FLIHVYASGEMWIRGDFMCKFRFSFHNLSSTILFCFSIFRCVVIHMSQESIKT 147
DB 88 LLVYIYANGDMFPSTVCKLVRFLEYNLCSTILFELCISVHRCGLVRLPHSIRMGRA 147
QY 148 RCAYVACAVWIIISLVAVIMPTFLITSTNRNRSACLDLTSDELNTIKMYNLITATF 207
DB 148 RYARVAVVWVVLACQAPVLYFTSVRGTRITCHDTSARELFSEHVAVASVWGLLE 207
QY 208 CLPLVIVLYCTTTIHTL-----THLOTDSCLEKQARLTIILLAFVYCFPHIL 260
DB 208 AVPSVYIIVCYLVARRLKLPAYGTGGLPR--AKRSVETIALVAVFALCELPFHT 264
QY 261 RVIRIESRLTISCSIEHQIEHAYIVSRPLAALNTPGULLY 302
DB 265 RTLYVSFRSLDLSCHITLNAIMAYKITRPLASANSCLDPVLY 306

Search completed: May 30, 2003, 13:45:04
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 30, 2003, 13:42:28 ; Search time 40 Seconds

(without alignments)
809.933 Million cell updates/sec

Title: US-10-023-775b-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANASDPDYAA.....RCKVSGNLBOAKKISYNNP 337

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR-73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567	32.0	373	2	JC4737
2	565.5	31.9	362	2	S33733
3	562	31.7	373	2	JC4162
4	514	29.0	365	2	S68679
5	479	27.0	373	2	A47556
6	438	24.7	375	2	A54946
7	423	23.9	328	2	I55450
8	419.5	23.7	420	2	I51667
9	405	22.9	328	2	JC4800
10	397	22.4	427	2	S17148
11	396.5	22.4	432	2	A43448
12	388.5	21.9	399	2	I48705
13	388.5	21.9	425	2	A37912
14	380	21.5	308	2	I50241
15	376.5	21.3	361	2	B45680
16	376.5	21.3	397	2	S66518
17	370	20.9	355	2	G02436
18	356	20.1	383	2	S55594
19	355	20.0	352	2	G00048
20	354	20.0	352	2	A45747
21	353	19.9	362	2	S68207
22	353	19.9	362	2	B57641
23	349.5	19.7	423	2	JC7677
24	349	19.7	356	2	S42096
25	348	19.6	354	2	I53033
26	348	19.6	362	2	A57641
27	347.5	19.6	363	2	A49092
28	346.5	19.6	344	2	T09508
29	345.5	19.5	363	2	I48261

30	344.5	19.5	378	2	B57335	lymphocyte-specific
31	344	19.4	353	2	JC2492	G protein-coupled
32	340	19.2	370	2	JC5549	hepatic P2Y5-
33	339.5	19.2	363	2	JC2543	angiotensin II rec
34	339	19.1	360	2	G02064	G protein-coupled
35	338.5	19.1	359	2	S15403	angiotensin II rec
36	337	19.0	353	2	S28787	neuropeptide Y/pep
37	336.5	19.0	360	2	A53611	interleukin-8 rece
38	336	19.0	362	2	JN0694	angiotensin II rec
39	334	18.9	356	2	I49340	MIP-1 alpha recept
40	332.5	18.8	355	2	JQ1231	chemokine (C-C) re
41	328	18.5	355	2	A45177	G protein-coupled
42	327	18.5	352	2	JC5067	G protein-coupled
43	327	18.5	387	2	I69202	G protein-coupled
44	326.5	18.4	378	2	A45680	angiotensin II rec
45	325.5	18.4	359	2	S44425	

ALIGNMENTS

RESULT 1

JC4737

G protein-coupled receptor P2Y1 - human

N:Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor

C:Species: Homo sapiens (man)

C>Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000

C/Accession: JC4737; JC4615; S54253

R:Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Boeynaems, J.

Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A>Title: Cloning and tissue distribution of the human P2Y1 receptor.

A:Reference number: JC4737; MUID:96205320; PMID:8650005

A:Accession: JC4737

A:Molecule type: DNA

A:Residues: 1-373 <JAN>

A/Cross-references: GB:S81950; NID:q1839438; PIDN:AA847091.1; PID:q1839439

R:Ayanathan, K.; Webb, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, Biochem. Biophys. Res. Commun. 218, 783-788, 1996

A>Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.

A:Reference number: JC4615; MUID:96158962; PMID:8579591

A:Accession: JC4615

A:Molecule type: mRNA

A:Residues: 1-373 <AVY>

A/Cross-references: GB:U42029; NID:q1147730; PIDN:AA97872.1; PID:q1147731

A:Experimental source: erythro leukemia cells

R:Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.

submitted to the EMBL Data Library, May 1995

A/Description: Cloning of a human putative P2Y receptor.

A:Reference number: S54253

A:Accession: S54253

A>Status: preliminary

A:Molecule type: mRNA

A/Residues: 1-137,139-373 <LEO>

A/Cross-references: EMBL:Z49205; NID:q798835; PIDN:CAA89066.1; PID:q798836

C/Comment: This receptor belongs to a family of G protein-coupled receptors. It resp

C/Genetics:

A:Gene: P2Y1; GDB:P2Y1

A/Cross-references: GDB:677125; OMIM:601167

A:Map position: 3pter-3qter

C/Superfamily: ATP receptor P2U

C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane i

F:52-77/Domain: transmembrane #status predicted <TM1>

F:88-111/Domain: transmembrane #status predicted <TM2>

F:124-152/Domain: transmembrane #status predicted <TM3>

F:171-191/Domain: transmembrane #status predicted <TM4>

F:214-237/Domain: transmembrane #status predicted <TM5>

F:261-282/Domain: transmembrane #status predicted <TM6>

F:305-328/Domain: transmembrane #status predicted <TM7>

F:11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status pre

F:330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pre

F:343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-d

	Matches	101, Conservative	64, Mismatches	119, Indels	4, Gaps	2
QY	26	DENLPKMHYLPVYIGIIFELVGFEGNNAVITYIKMRPMKSSITIMLNLA	CTDLLYLS	85		
	30	DED--FFKILLPVSAVAVEVGLGNAATPLMEIFRLPMDATAYMHMLASD	LLDYLS	87		
Db	86	LPFLIHVYASGEMNIFGDFMCKFIREFSEFNLYSSILFLCFISIRYCVII	HPMCSFIH	145		
QY	88	LPTLIYYAAHNHMPFEGTEICKFVRFELFYMNLYSVLETLTCISVHR	YLGICHPDLALRMG	147		
Db	146	KTRBAVAVACAVYMIISLVAVIPMFLLSTRTKINSACLDLTSDELNTIK	YNIILRAF	205		
QY	148	RPRLAGLCLCAVNLVAVACGLVPMLEFVYTSKNGTIVLDHDTTPREFDH	YVSSAVMGL	207		
Db	206	TECLPELVIVTLCTYTIHHTLHGL--QTDSCIKOKARRLLTILLAFYVC	LPFHILRAY	263		
QY	208	LFQVDCVLTVCYGLMARLKYQPLPGSQAQSSSRLLSRITIAVLTVAFNC	VEVPFHITRTI	267		
Db	264	RIESRLTISCSIEINOHEAVYSRPLAALMTFGLLLYVYVSDNQ	311			
QY	268	YYLARLEADCRVLNIVYVYKTVIRPLASNSCSDPVLYKLLGDKYR	315			

RESULT 5
A47556
ATP receptor P2u - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: A47556
R:Jushty, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A:Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells
A:Reference number: A47556; MID:9328107; PMID:7685114
A:Accession: A47556
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373 <LUS>
A:Cross-references: GB:114751; NID:g309457; PIDN:AAA39871.1; PID:g309458
C:Superfamily: ATP receptor P2u
C:Keywords: transmembrane protein

Query Match	27.0%	Score 479;	DB 2;	Length 373;
Best Local Similarity	34.4%	Pred. No. 6e-34;		
Matches	97;	Conservative	58;	Mismatches 117; Indels 10; Gaps 2
QY	28	NIPKMHLYVYIGIIFLVGEPGNAVSYIYIEKMRPMKSSITIMLNACTDLYLTSLP	87	
Db	28	NEDKRYLLLPVSYGVVCLGLCLNVAALYIEFLCKLTNNASTYTFHFLVASLSTLAASLP	87	
QY	88	FLIHVYASGEWMIFGDFMCKEFLRFSEFHNELSSILFLCFSEFRFCVIIHPMSPCSIHKT	147	
Db	88	LLVYTYANGDHMPSTVYCKLVRFLFYTNLYCSILFLFCISVHRCLGVAPRLHSLRMGSA	147	
QY	148	RCAYVACAVNVIISLVAVIYPMFTILTSNTRKSCALDITSSDELNTIKWYLLPATTF	207	
Db	148	RYARRVAAVVWVLYLACQAPVLYETTSVTRGTRICHTPSAEELSHFVAYSVMGLIF	207	
QY	208	CLPIVYVLCYTTIIITHTL-----THSLQTEDSCSKOKARRTIILLAFYVCPPEHIL	260	
Db	208	AVPSPVILVYCVLMARRLKPRAYGTTGLPR--AKRSRVRIALVLAVFALCPLEPHYT	264	
QY	261	RVIRIESRLISCSIEHQIHDAIYVSRPRLAALNFGNLLY	302	
Db	265	RTLYYSFERSLDLSCHTLLAINNAKYITPRPLSANSCLDPVLY	306	

RESULT 6
A54946
P-2U nucleotide receptor - human
C:Species: Homo sapiens (man)
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
C:Accession: A54946
R:Par, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.

Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994
A:Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cys
A:Reference number: A54946; MUID:94211846; PMID:8159738
A:Accession: A54946
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-375 <PAR>
A:Cross-references: GB:007225
A:Note: parts of this sequence were confirmed by protein sequencing
C:Genetics:
A:Gene: GDB:P2RX2, HP2U, P2U
A:Cross-references: GDB:362713; OMIM:600041
A:Map position: 11q13.5-11q14.1
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 24.7%; Score 438; DB 2; Length 375;
Best Local Similarity 33.0%; Pred. No. 2,1e-30;
Matches 93; Conservative 59; Mismatches 118; Indels 12; Gaps 4;

Query Match	24.7%	Score 438	DB 2	Length 375
Best Local Similarity	23.0%	Pred. No. 2,1e-30		
Matches	93	Conservative	59	Mismatches 118; Indels 12; Gaps 4
QY	28	NIPLMHMYIPVYIGILFLVGFPGNAVISTYIFKMRPMKSSITIMLNACTDILYITSLP	87	
DB	28	::: ::: ::: :::	87	
	28	NEDFVYLLIPSYGVAVCVGLCLNMAAGLIFLCRLTKMASTYTMHLLVASDLVYASLP	87	
QY	88	FLIHKYASGEMNIFEDFMCKFTRFSEHMYLSILFLTCFSIFRYCVIIHPMSCFSIHKT	147	
DB	88	::: ::: ::: :::	147	
	88	LLVYYTARODHMFSTVLCKLVRFLFYTLNYLCSILFLTCISVHRKGLGVLRPLRSRLRWGR	147	
QY	148	RCAYVAGAVMMIISLVAVIPMTFLITSTNTRNSACLDLTSSDELNTIKMYNLINATTF	207	
DB	148	::: ::: ::: :::	206	
	148	FRARVAGAVMWLVLAQCAPVLYEYVTSNR-GLPTCHDTSAPLRSRYAVASVMGLLE	206	
QY	208	CLPLVIVTLCYTTIIHTL-----THGQDTSCLKQKARRLTILLLAFVYCCFPHIL	260	
DB	207	::: ::: ::: :::	263	
	207	AVPFVAVIIVCYVLMARRLKLKPAYGTSGGPR--AKKRSVRIAVLVLAWFALCFPHVT	263	
QY	261	PIRIRIESRLTSCISCIENQIHQAVYSRPLALNFGNLLI	302	
DB	264	::: ::: ::: :::	304	
	264	KLIYYSRSLDLSCHTLLNAINNAVYTR--IASANSCLDPEVLY	304	

```

      RESULT 7
      155450
      G protein-coupled p2 receptor - rat
      C:Species: Rattus norvegicus (Norway rat)
      C>Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 19-May-2000
      C:Accession: I55450
      R.Chang, K.; Hanaoka, K.; Kunada, M.; Takuwa, Y.
      J. Biol. Chem. 270, 26152-26158, 1995
      A>Title: Molecular cloning and functional analysis of a novel p2 nucleotide re
      A:Reference number: I55450; MUID:96064682; PMID:7592819
      A:Accession: I55450
      A>Status: preliminary; translated from GB/EMBL/DDBJ
      A:Molecule type: mRNA
      A:Residues: 1-328 <RES>
      A:Cross-references: GB:D63665; NID:g1066007; PIDN:BAA09616.1; PID:g1066008
      C:Superfamily: ATP receptor P2u
      C:Keywords: G protein-coupled receptor

Query Match          23.9%; Score 423; DB 2; Length 328;
Best Local Similarity 32.9%; Pred. No. 3.7e-29;
Matches 96; Conservative 44; Mismatches 126; Indels 26; Gaps 5

QY      36 LPVYIGILFLVFPGGNAYISTIRKMRPKSKSTIIMLNLACTDLLYLTSPLLIHYAS 95
       1 : : : : : | | : : : : : | | | | | | | | | | | | | | | | |
Db      29 LPPVSYVALVLGDLPNVCVIAGICASRRLTSAVYTLLMLADLADLCSPILLIYYNR 88
       1 : : : : : | | : : : : : | | | | | | | | | | | | | | | | |
QY      96 GENNIIFGDPMCKFIREFSFHFNLYSSILFETCFESIFRYCVIIHPMSCFSIHK--TRCAYV 152
       1 : | | | | | : : : | | : | | | | | | | | | | | | | | | | |
Db      89 GDHWFGDGLACRLVRFLEFYANLHGSIILFTCLISFQRYLGICHPAPW--HKRGGRRAAV 146
       1 : | | | | | : : | | : : : | | : | | | | | | | | | | | | | |
QY      153 ACAVAWIISLVAVIPMTFLTITSTNKTRNSKACDLRSSDELNTIKYNLTATFTCPLEPV 212
       1 : | | | | | : : | | : : : | | : | | | | | | | | | | | | | |

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Db 147 VCGVWLVVTAQCLPFAVFAATGQIRNFTVCYDLSPPILSTRVLPYGMALTVIGFLPEFT 206
 Qy 213 IVTLCTYTIHTLHGLQTDSC-----LKQKARLTLLLLAFYVCELPFHIL 260
 Db 207 ALLACCYCRMARRL-----CRQDGPAGVPAQGRSRAAMAVVAVVAVFISLPFHIT 258
 Qy 261 RVIIIESRL-SIGCSINQIHEHYISRPALANTFQNLILVYVSDNFOQ 311
 Db 259 KTAVALAVSTPGVSCPVLEFPAAVYKGRFPASANSVLDPLTFYFTQCKFR 310

RESULT 8

151667
 thrombin receptor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

R:Gerszten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanavicz, T.; Turck, C.W.; Vu, T.H.; C
 A:Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac
 A:Reference number: 151667; MUID:94195429; PMID:8145852
 A:Accession: 151667
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-420 <GER>

Cross-References: EMBL:U09632; NID:9495197; PIDN:AAAI8498.1; PID:9495198

Query Match 23.7%; Score 419.5; DB 2; Length 420;
 Best Local Similarity 31.1%; Pred. No. 9,66-29;
 Matches 93; Conservative 73; Mismatches 108; Indels 25; Gaps 7;

Qy 35 YLPIVYGIIFLVGPGNAVISTYIFKMRPKSSTIIMNLACDLYLSLPLIHXA 94
 Db 103 FVPLVYVIVVGVPLNLIIIFLKKYKRPVAVVLAIDLADLVSVLPKXIAHL 162
 Qy 95 SGEMWIDGDFCKIRSFHNLSSILFLCFISFRCAVYIHHMCSGSIHKTKCAVYAC 154
 Db 163 SGNDMLFGPGKCRVLTALFYCMYCSVLLASISVDRLAVVPMHSLSWRTMSRAYAC 222
 Qy 155 AVWIIISLVAVIPMTFLTSTNTRNSACDLTSDDELNTK----WYLLITATTECL- 209
 Db 223 SFWILISIASITPLV----TEQTKIPRLDITTCHEVDLKDLDKDF--IYFSSRCLL 276
 Qy 210 ----PLVIVLCYTTIHTLHGLQTDSCQKARRLTLLLLAFYVCELPFHILRYIRI 265
 Db 277 FFEVPIITITTCYIGIRLSISSSIENSCCKTRALFLAVVLCYFIICFPTNVL----- 331
 Qy 266 ESRLISISCSINQ-IHEAVYISRPALANTFQNLILVYVSDNFOQAVCTVRC-KYS 322
 Db 332 ----FLTHYLOEANEFLYFAIYLSACVGSVSCDPLIYYASVOCQRYLSLCCRRVS 387

RESULT 9

151667
 P2Y6 receptor - human

C:Species: Homo sapiens (man)
 C:Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000

C:Accession: J04800; G02514
 R:Communi, D.; Parmentier, M.; Boeynaems, J.M.
 Biochem. Biophys. Res. Commun. 222, 303-308, 1996
 A:Title: Cloning, functional expression and tissue distribution of the human P2Y6 recept
 A:Reference number: J04800; MUID:96222498; PMID:8670200
 A:Accession: J04800
 A:Molecule type: mRNA
 A:Residues: 1-328 <COM>

A:Cross-References: EMBL:X97058

A:Experimental source: Placenta

R:Hammer, F.; Southey, M.C.; Somers, G.R.; Hutchins, A.M.; Venter, D.J.
 submitted to the EMBL Data Library, March 1996

A:Reference number: H01373

A:Accession: G02514

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 'W',4-328 <HAM>
 A:Cross-References: EMBL:U052464; NID:91407632; PIDN:AA03572.1; PID:91407633
 C:Genetics:
 A:Gene: P2Y6
 C:Superfamily: ATP receptor P2u
 C:Keywords: glycoprotein; placenta; receptor; transmembrane protein
 F:26-52/Domain: transmembrane #status predicted <TM1>
 F:63-86/Domain: transmembrane #status predicted <TM2>
 F:104-122/Domain: transmembrane #status predicted <TM3>
 F:143-167/Domain: transmembrane #status predicted <TM4>
 F:193-216/Domain: transmembrane #status predicted <TM5>
 F:241-264/Domain: transmembrane #status predicted <TM6>
 F:283-305/Domain: transmembrane #status predicted <TM7>
 F:5,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.9%; Score 405; DB 2; Length 328;
 Best Local Similarity 32.6%; Pred. No. 1,36-27;
 Matches 94; Conservative 44; Mismatches 140; Indels 10; Gaps 4;

Qy 32 KMAYLPVYGIIFLVGPGNAVISTYIFKMRPKSSTIIMNLACDLYLSLPLIH 91
 Db 25 KOLLPPVYSAVLAAGPLNLCVITQICTSRRLTRAVVTLNLADLLYACSLPLIY 84
 Qy 92 YVAGEMWIRGDFCKIRSFHNLSSILFLCFISFRCAVYIHHMCSGSIHK---TR 148
 Db 85 NYAGDHPFDFGFCRVLVRFYANLHGSILFLCFISFRCAVYIHHMCSGSIHK---TR 142
 Qy 149 CAVAVCAVWIIISLVAVIPMTFLTSTNTRNSACDLTSDDELNTKMYNLITATTEFC 208
 Db 143 AAMLVCAVWLAVALTQCLPRAIFAATGQIRNFTVCYDLSPPALATHMPGALTIVGL 202
 Qy 209 LPLVIVLCYTTIHTLHGLQTDSCQKQ-----KARRLTLLLLAFYVCELPFHILVIR 264
 Db 203 LPFAALACVCLLACRLCRQDGPAPVPAQGRSRAAMAVVAVVAVFISLPFHITRTAY 262
 Qy 265 IESRL-SIGCSINQIHEAVYISRPALANTFQNLILVYVSDNFOQ 311
 Db 263 LAVSTPGVPCVLEAFPAVYKGRFPASANSVLDPLTFYFTQCKFR 310

RESULT 10

1517148
 alpha-thrombin receptor - Chinese hamster

C:Species: Citellus griseus (Chinese hamster)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: S17148
 R:Rasmussen, U.B.; Youret-Craviari, V.; Jallat, S.; Schlesinger, Y.; Pages, G.; Pavir
 FEBS Lett. 288, 123-128, 1991
 A:Title: cDNA cloning and expression of a hamster alpha-thrombin receptor coupled to
 A:Reference number: S17148; MUID:91348247; PMID:1652467
 A:Accession: S17148
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-427 <RAS>

A:Cross-References: EMBL:X61958; NID:9940495; PIDN:CAAA3957.1; PID:949538
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.4%; Score 397; DB 2; Length 427;
 Best Local Similarity 28.4%; Pred. No. 8,76-27;
 Matches 95; Conservative 75; Mismatches 141; Indels 24; Gaps 6;

Qy 10 NASDPDYAAFGNCTDENIPLKMH-----YLPVYGIIFLVGPGNAV 53
 Db 65 NESFLPGRALYLNKSHSPAPLAFISDASGYLSPMLRLFLPSVYTFEVVSLPLNL 124
 Qy 54 VISYIIRKMRPKSSTIIMNLACTDLYLITSLPLIHYYASGEMWIRGDFCKIRSF 113
 Db 125 AIAVEVLMKMRPKVPAVYVLMHLMADLVFVSVLPKISYFSGSDWQFGSGMCRFATAAF 184
 Qy 114 HFNYSILFLCFISFRCAVYIHHMCSGSIHKTRCAVAVCAVWIIISLVAVIPMTFLT 173
 Db 185 YCNMTASIMLTATISIDRLAVVYPIOSLSWRLGRANFTCLIVWALINGVPL-LIKE 243

Db 281 VPLISTFCVYIIIRCLSSSAVANRSKSRALFLSAAFICFIIFCGEPTNLLTAHYS-- 338
 OY 269 LLSICSTENQIHEAYISRPLALNTEGNTLLVYVSDNQAVCSYVRCK----- 320
 Db 339 FLSTSTTE-AAFAYILCVCVSSISCSIDPLIYVYASSECORYVSTLCKESSDPSSY 397
 OY 321 -VSGNLEQAKKISYSNN 336
 Db 398 NSSGOLMAKMDTCSSN 414

RESULT 14

150241
 G:protein-coupled receptor 6H1 - chicken
 N:Alternate names: purinoceptor 6H1
 C:Species: Gallus gallus (chicken)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000
 C:Accession: 150241; J04618
 R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
 J:Immunol. 151, 628-636, 1993
 A:Title: Identification of a G protein coupled receptor induced in activated T cells.
 A:Reference number: 150241; MUID:9332058; PMID:8393036
 A:Accession: 150241
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-308 <KAP>
 A:Cross-references: GB:J06109; NID:9304383; PIDN:AB06587.1; PID:9304384
 R:Meib, T.E.; Kaplan, M.G.; Barnard, E.A.
 Biochem. Biophys. Res. Commun. 219, 105-110, 1996
 A:Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
 A:Reference number: J04618; MUID:96190677; PMID:8619790
 A:Accession: J04618
 A:Molecule type: mRNA
 A:Residues: 1-308 <MEB>
 A:Cross-references: GB:J06109; NID:9304383; PIDN:AB06587.1; PID:9304384
 A:Experimental source: T-cells
 C:Comment: This receptor plays a role in T-cell activation.
 C:Genetics:
 A:Gene: P2Y5
 C:Superfamily: ATP receptor P2u
 C:Keywords: G protein-coupled receptor; transmembrane protein
 F:15-40/Domain: transmembrane #status predicted <TM1>
 F:51-74/Domain: transmembrane #status predicted <TM2>
 F:89-109/Domain: transmembrane #status predicted <TM3>
 F:133-153/Domain: transmembrane #status predicted <TM4>
 F:177-201/Domain: transmembrane #status predicted <TM5>
 F:227-248/Domain: transmembrane #status predicted <TM6>
 F:269-292/Domain: transmembrane #status predicted <TM7>

Query Match 21.5%; Score 380; DB 2; Length 308;

Best Local Similarity 30.8%; Pred. No. 1.8e-25;

Matches 90; Conservative 58; Mismatches 134; Indels 10; Gaps 6;

OY 23 NCNDENPLKMHLYPIVYIGILVGFPGNAVISTYIFKAPKMSSTITIMINACTDLY 82
 Db 5 NCSTED-SFRYYLYGCVFVGLIACVAIYIFFTLKVRNETTYMMLAISDLF 63
 OY 83 LLSLPLIHYASGENIFEDFMCKEIRFSFHELYSILFLCFESIFRCVITHPMSCF 142
 Db 64 VFLPFRYYFV-RNMPEDVCKISVTLFYTNMYSILFLICISYDRFLAYHPRSK 122
 OY 143 SIHTRCAVAVAVIISLVAVIMPTFLTSTNRTNSACLDLTSSDELNTIKW---- 198
 Db 123 TLTKRNARIYCAVAVITVLAGSPASF-POSTRNQNTEDRCFENPESTMTYLSRI 181
 OY 199 NLILFATTECLPLVYILCTTIIHTLH--GLQTSCLQKARRLTILLALFYVFLP 256
 Db 182 VIFIEIVGFPIPLNLTCTVLRNLKPLTSLRNKLSKKVLMIFVHIVFCFCFVP 241
 OY 257 FHLIRVIRISRLS--ISCSIEQIHEAYISRPLALNTEGNTLLVYVSD 307
 Db 242 YNTLLIYSIMRTQWINC SVAVATRTMYPVTLICIAVSNCCFDEIYVFTSD 293

RESULT 15

B45680
 G:protein-coupled peptide receptor EBI 2 - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
 C:Accession: B45680
 R:Birkenbach, M.; Josefsen, K.; Yalamanchilli, R.; Lenoir, G.; Kieff, E.
 J:Virol. 67, 2209-2220, 1993
 A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple
 A:Reference number: A45680; MUID:93188173; PMID:8363238
 A:Accession: B45680
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-361 <BIR>
 A:Cross-references: GB:L08177; NID:9292056; PIDN:AAA3924.1; PID:9292057
 A:Experimental source: B-lymphocytes
 A:Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBI:127097)
 C:Superfamily: ATP receptor P2u
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 21.3%; Score 376.5; DB 2; Length 361;

Best Local Similarity 26.9%; Pred. No. 4.3e-25;

Matches 92; Conservative 70; Mismatches 159; Indels 21; Gaps 7;

OY 11 ASDF-PDYAAFGNCTDENIPDKMHY-----LPYVIGILVGFPGNAVISTYIFKMR 63
 Db 6 ANNTFSAIPQSGNDGCD-----LVNHSSTARVMPHLHSVFIIGLVGNLALVYVQNRK 61
 OY 64 PKMSSTITIMINACTDLYLTSPLFLIHYASGENMIFGDMCKEIRFSFHELYSILF 123
 Db 62 KINSTLYSNLVISDILFTTALPTRIAYYAMGDFMRIGDALCRITAVEYINTYAGVNF 121
 OY 124 LTCFSIRYCVIIHPMCSFSLHKTROCAVAVAVIISLVAVIMPTFLTSTNRTNSAC 183
 Db 122 MTCISDRFAVAVHPLNKNKIRLEHAKGVCIFWMLVPAQTLPLINPMKQDAERTTC 181
 OY 184 LDLTSSDELNTIKWYNDILATTECLPLVITVLTCTYTIHTL-----THGLQTSCLQK 238
 Db 182 MEYNPFEETKSLPILLGACFIGVPLIIILICYSQICKLRTAKQNLFTEKSGVNRK 241
 OY 239 ARRLTILLALFYVCLPFLHILVIRIESRLSISCSIF-NQIHEAYISRPLALNTFG 297
 Db 242 ALMTIIILIVFVLCFEPYHV-AIIQHMIRKLFESNLFESQHSFQISLHFTVCLMNFN 300
 OY 298 ---NLIVYVSDNQOAVCSYVRCKYSGMLEQAKKISYSNN 336
 Db 301 CNDPFLYFRACKGYKRWMLKROVSVSISSAVSAPDEN 342

Search completed: May 30, 2003, 13:47:20
 Job time: 42 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: May 29, 2003, 23:40:20 ; Search time 1706 Seconds
(without alignments)
3199.226 Million cell updates/sec

Title: US-10-023-775b-2
Perfect score: 1771
Sequence: 1 MNEPLDYLANASDFPDYAAA.....RCVSGNLEQAKKISYNNP 337

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US10023775/runat_23052003_160018_12459/app_query.fasta_1.519
-DB=EST -OFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -DIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEA=SITE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=us10023775.qcgn1.1.1906.etrnat.23052003.160018.12459 -NCPU=6 -ICPU=3
-NC_MMAP -LARGEQUERY -NEG.SCOES=0 -WAIT -DSPBLOCK=100 -LONKLOC
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estinu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gsa:*
18: em_gsa_hum:*
19: em_gsa_inv:*
20: em_gsa_pln:*
21: em_gsa_vrt:*
22: em_gsa_fun:*
23: em_gsa_mam:*
24: em_gsa_mus:*
25: em_gsa_other:*
26: em_gsa_pro:*
27: em_gsa_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	478	27.0	2542	11	AK017378	AK017378 Mus muscu
2	478	27.0	3001	11	AK005013	AK005013 Mus muscu
3	400	22.6	744	14	BM723768	BM723768 UI-E-EOL-
4	399	22.5	956	17	CNE602847	AL186585 Tetraodon
5	399	22.5	1101	17	CNE044V3	AL109576 Tetraodon
6	395.5	22.3	3005	14	AK019478	AK019478 Mus muscu
7	388	21.9	623	14	B0038875	B0038875 pgnlc.pko
8	371.5	21.0	821	14	BM946831	BM946831 UI-M-EHOP
9	370.5	20.9	2020	11	BC013202	BC013202 Homo sapi
10	370	20.9	971	9	AU091121	AU091121 AU091121
11	367.5	20.8	946	9	AL551903	AL551903 AL551903
12	366.5	20.7	904	9	AL532537	AL532537 AL532537
13	366.5	20.7	931	9	AL547762	AL547762 AL547762
14	353	19.9	641	14	B0396255	B0396255 NISC.ng19
15	352	19.9	638	9	AL675845	AL675845 AL675845
16	348	19.6	1101	17	CNE60532S	AL18925 Tetraodon
17	336.5	19.0	1739	11	AK008997	AK008997 Mus muscu
18	334.5	18.9	789	12	BG205056	BG205056 RST24475
19	334	18.9	765	13	B1183645	B1183645 UNL-P-FN-
20	333	18.8	734	13	BG914321	BG914321 602810633
21	332.5	18.8	851	13	B1833118	B1833118 603090834
22	331	18.7	1051	13	BM545259	BM545259 AGENCOURT
23	330.5	18.7	1026	17	CNE051MY	AL317059 Tetraodon
24	323.5	18.3	613	9	AL657842	AL657842 AL657842
25	321.5	18.2	1063	14	BM918491	BM918491 AGENCOURT
26	319.5	18.0	861	13	B1768868	B1768868 603057774
27	319.5	18.0	1088	13	BM549799	BM549799 AGENCOURT
28	319.5	18.0	1766	11	AK008952	AK008952 Mus muscu
29	318.5	18.0	606	17	AZ953874	AZ953874 2M0219117
30	318.5	18.0	663	13	BM426517	BM426517 pfgfn.pko
31	317	17.9	2146	11	BC027965	BC027965 Homo sapi
32	315	17.8	884	12	BG182330	BG182330 RST1196 A
33	311	17.6	938	17	CNS04SUP	AL305672 Tetraodon
34	311	17.6	1048	11	AK011967	AK011967 Mus muscu
35	309.5	17.5	1063	14	BM920158	BM920158 AGENCOURT
36	309	17.4	620	13	B1961697	B1961697 MONO1.3.D
37	307	17.3	1074	14	BM917063	BM917063 AGENCOURT
38	306	17.3	989	17	CNE03C14	AL237227 Tetraodon
39	305	17.2	808	9	AJ456719	AJ456719 AJ456719
40	303	17.1	741	9	AJ453402	AJ453402 AJ453402
41	302.5	17.1	766	9	AJ450835	AJ450835 AJ450835
42	301	17.0	876	13	B1906283	B1906283 603063222
43	300.5	17.0	1076	14	BM923028	BM923028 AGENCOURT
44	299	16.9	800	9	AJ452624	AJ452624 AJ452624
45	299	16.9	885	9	AL546894	AL546894 AL546894

ALIGNMENTS

RESULT 1
AK017378
LOCUS
DEFINITION
AK017378 2542 bp mRNA linear HTC 19-JAN-2002
Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
library, clone:5430432J15;purified receptor p2y, G-protein
coupled 2, full insert sequence.

ACCESSION
AK017378
VERSION
AK017378.1 GI:12856588
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (strain:C57BL/6J) 6 days neonate head cDNA to mRNA,
clone:lib-Riken full-length enriched mouse cDNA library
clone:5430432J15.

ORGANISM
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
99279253
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishibe, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunori, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
20530913
4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, K., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, K., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kusukawa, T., Saito, R., Kaoto, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischer, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamliya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyokawa, K., Wang, K. H., Weitz, C., Wittke, C., Wilming, L., Wysshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
21085660
5 (bases 1 to 2542)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Areakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kusukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, Y., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quekembush, J., Saito, H., Saito, R., Sasaki, C., Sasaki, K., Sano, H., Sasaki, D., Schraml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sobabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamana, K., I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (10-JUL-2000) yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222).

COMMENT

Fax: 81-45-503-9216)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research at Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGGAGAACAATTCACGTAAATTATAATCATCCCCCCCCTCC 3'] cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'

FEATURES

SOURCE	Location/Qualifiers 1..2542 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="FANTOM_DB:5430432j15" /db_xref="MGD:MGI:1897121" /db_xref="taxon:10090" (clone="5430432j15" /tissue_type="head" /clome_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="6 days neonate" 1..2542 /gene="Pzry2" 484..1605 /gene="Pzry2" /note="data source: MGD, source key: MGI:105107, evidence: ISS purinergic receptor P2Y ₂ , G-protein coupled 2 putative" /codon_start=1 /protein_id="BAB30719.1" /db_xref="GI:12856589" /db_xref="MGD:MGI:105107"	 end: BamHI; Host: DH10B.
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gene

CDS

```

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BASE COUNT      517 a       737 c     705 g       582 t         1 others
ORIGIN
Alignment Scores:
Pred. No.:          2.66e+41           Length:        2542
Score:              478.00             Matches:         97
Percent Similarity: 54.96%            Conservative:    58
Best local Similarity: 34.40%          mismatches:     117
Query Match:        26.99%             Indels:         10
DB:                 11                gaps:          2

US-10-023-775B-2 (1-337) x AK017378 (1-2542)
Oy   28 AsnllleProLeuUysMeThIStyrLeuProValIlleTygAllyllelePeHeLeuValgly 47
Db   565 AACGAGACTTCAAAGTGCGTGCTGCCTGATATCTCTAATGCCGCTCAAACCtGAACGCC 624
Oy   48 PhnePrOGLySnalavallleserThrTyrrilePhelaysmetaGrProtPysser 67
Db   625 TTGTGCTGAACGTGCGTCTCTATATCTCTATATGCCGCTCAAACCtGAACGCC 684
Oy   SerThrilleMetleUsanleUAalaCyStrAspleuleuryleuThrSerleupro 87
Db   685 TTCACACACCTACATGTTTTCACCTGGACGTTTGGACCTCTCTTAAGCAGAGCGCTCCGCGG 744

```


OY		88	PheUleuHISLSTYRTYLALASerGILVALusnRPrIlepeegLYAsPHeMeCyslys	107
Db		745	CTGTGGTTATTTACTACAGCCCGGGGGTACCATTGGCCATTAGCACGGTCCTGCAG	804
OY		108	PheIIeargPHeSerPHeHISPhEasnuLeuTySeriLeuPheLeuThrCysDhe	127
Db		805	CTGGAGCTTGTCCTTCTTACACAACACTCTACAGACANCTCTTCTTCACTGCATC	864
OY		128	SerIlePHeaRgtTYRCysValIleIleHISProMetSerCysPHeSerIleHISlyThr	147
Db		865	AGCGTGAACCCGGTCGTGGAGTCTCGGCCCTCTGCATCCCTGCCTTGGGGCGGGCC	924
OY		148	ArgcysAlaValAlaIacysAlaValAlPrIleIleSerIeueValAlaValIlepro	167
Db		925	CATTATGCCCCCGGGGTGGCTGGCTGTGTGTGGGGTGGTGGCTGCAGGACCC	984
OY		168	MethTrPHeuIleIeThrSerThraAsnrgThraAsnArserAlAcysLeuaSPHeuThr	187
Db		985	TGTGCTCATCTTCGTCACACCAAGGGTGGGGAAACCGGANCACTTGCANAGAACCTCG	1044
OY		188	SerSeraspGIuleuAsnThrlIelystTPyrAsnLeuIleLeuThAlaThrThrphe	207
Db		1045	GCCCCAGAGCTCTTAGCCATTGTTGGCTTACAGCTCCGTCAGCTGGTCTGCTTTT	1104
OY		208	CysLeuPProLeuValIleValThrlencysThrThrlIleIleHISThleu-----	225
Db		1105	GCTGTGCCCTTTCCGNATCCCTGGTCTGTTAAGCTGCTTAAGGCCAGGCGGTCTGCAA	1164
OY		226	-----ThrlsGLyLeugInThraSPserCysLeuLySGlnLysAlarG	240
Db		1165	COGGTTATGGGACCACAGAGAGTCTGCTCGG-----GCCAAGCGCAAGTCTGTG	1215
OY		241	ArgLeuthrlIleLeuLeuLeuAlaPheTyValCysPHeLeuProPHeHISlleLeu	260
Db		1216	CGCACCAATGGCTGTGGTACTGGCGGTCTTCCGCTCTGCTCTGCTTCCATCCACTCAG	1275
OY		261	ArgvalIleArgIleIeuserArgLeuLeuSerIleSerCysSerIleIeuanGlnIle	280
Db		1276	CGCACCCCTACTACTCTCTCCGATCATCTACCTACCTACCTCCACACACCCCTCAGATC	1335
OY		281	HISgluaIaTyrlIeValSerArgProbeuAlaIaleuAsnThrPheGLYAsnLeuLeu	300
Db		1336	AACATGGCATTAAGATACCCCGCGCTGGGCCACAGCCCAACAGTGTCTTGACCCGGTA	1395
Y		301	LeuTYr 302	
Db		1396	CTCTAC 1401	
RESULT 2				
AK005013				
LOCUS				
DEFINITION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
AUTHORS				
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JOURNAL
MEDLINE
PUBMED
11042159

REFERENCE
AUTHORS

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunishi, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaiguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Kameda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsutani, S., Kawai, J., Okezaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
11076861

REFERENCE
AUTHORS

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kusunaga, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalova, S., Casavani, T., Flischiann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nakai, I., Resole, G., Quackenbush, J., Schriml, L.M., Staudt, F., Suzuki, R., Tomita, M., Wagner, E., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsch, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Garbolino, M., Gustincich, S., Hill, D., Hotman, M., Hume, D.A., Kamliya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, T., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyokawa, K., Wang, K.H., Weitz, C., Wittaker, C., Wilming, L., Wyszynski, B., Yoshida, K., Hasegawa, Y., Kawai, H., Kontsuki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

JOURNAL
MEDLINE
PUBMED
11217851

REFERENCE
AUTHORS

5 (bases 1 to 3001)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Aizawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Yamamoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Konda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numata, K., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toyokawa, T., Yamamura, T., Yamana, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Shuho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCCGCACTCGAGATTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase

FEATURES

Seq primer: M13 Reverse.
Location/Qualifiers

1..744
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/db_xref="taxon:9606"
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/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-EO1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this library is CCGGATAC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 217 a 168 c 126 g 233 t
ORIGIN

Alignment Scores:

Pred. No.: 1.59e-33 Length: 744
Score: 400.00 Matches: 80
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.59% Indels: 0
DB: 14 Gaps: 0

US-10-023-775b-2 (1-337) x BM723768 (1-744)

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DB 61 AATCAGATCCATGACCTTACATCGTTTCTAGACCTTACGCTCTGACACCTTGGT 120
QY 298 Aen1leu1leu1tyr1val1val1val1ser1asp1asn1phe1ng1lna1ala1cys1ser1th1val 317
DB 121 AACCTGTACTATATGTGTGTGTCAGCAGCAACTTTCACAGCGCTGTGCTCAACAGTG 180
QY 318 Argcys1lyval1ser1cys1leu1glu1lna1al1al1cys1leu1ser1th1asn1pro 337
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RESULT 4

CNS028Y4/C

DEFINITION Tetradon nigriviridis genome survey sequence PUC-ori end of clone 245p17 of library G from Tetradon nigriviridis, genomic survey sequence.

ACCESSION AL186565
VERSION AL186565.1 GI:7824669
KEYWORDS GSS: genome survey sequence.
SOURCE Tetradon nigriviridis.
ORGANISM Tetradon nigriviridis

REFERENCE 1 (bases 1 to 956)
AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brothier,P., Quetier,F.,

TITLE

Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetradon nigriviridis DNA sequence

JOURNAL

Unpublished
2 (bases 1 to 956)

REFERENCE

Roest-Crollius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigriviridis

JOURNAL

Unpublished
3 (bases 1 to 956)

REFERENCE

Genoscope.
Direct Submission
Submitted (12-APR-2000)

COMMENT

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigriviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetradon>.

FEATURES

location/Qualifiers

1..956
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/clone="245p17"
/clone_lib="G"
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BASE COUNT 251 a 214 c 290 g 176 t 25 others
ORIGIN

Alignment Scores:

Pred. No.: 3.03e-33 Length: 956
Score: 399.00 Matches: 101
Percent Similarity: 51.55% Conservative: 65
Best Local Similarity: 31.37% Mismatches: 129
Query Match: 22.53% Indels: 27
DB: 17 Gaps: 10

US-10-023-775b-2 (1-337) x CNS028Y4 (1-956)

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QY 23 -----Asncys1thrasp1gua1n1le1pro1eul1ys1meth1s1ry1leu1pro1val 38
DB 901 TCAAGCTGTATATATTGTACAAATATCGAATCTTACTGAGAGTACTTCTGCCACCC 842
QY 39 I1etYg1Y11et1lePhe1leu1a1Gly1phe1Pro1Gly1Asn1a1a1Val1le1ser1Th1ry 58
DB 841 TTCTACGCTGTGAGAGTTCGCCGCGGTTTCCCGGACCTGTGGTGTCTTCTTGGTTAC 782
QY 59 I1ePhe1ys1Met1arg1Pro1Trp1ly1ser1Ser1Thr1le1Met1leu1asn1leu1a1cys1thr 78
DB 781 ATATTGTGCTTGCACAGTGTGCGACAGCTCCATATCTACTCTTCAACCTGGCCGTCTCA 722
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DB 661 ----CTAAACAGTCCCTTCTCTGTCATCGCAACCGCTATATCTGACGTCACCACTTAC 605
QY 119 Ser1Ser1I1ePhe1leu1Th1ry1cys1Phe1Ser1I1ePhe1Arg1Ty1r1Cys1Val1I1eH1s1Pr 138
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DB 544 GACGCGGAACCACTACTCTGTAACCGGCGGGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 485
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      424 GKMAACTGAMACAGTGTAAAGGACTTCTCCAGCTTAAGGAGACTCAACACTTTGCT 365
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      231 RAspSerCysLeuLysGlnLysAlaArgArgLeuThrIleLeuLeuLeuAlaPheTy 251
      253 CAGAGCCACATCTGTTCAAGCGCCCATCAGGGTGTGCTGTATMTGCAGCCATATTCCT 194
      251 rValCysPheLeuProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeu 271
      193 GGTCTCTCTTACACCCATACACGATGAGAGAACATTAATAATCGCTCTCAGAGGTTTG 134
      271 rIleSer-----CysSerIleGluAsnGlnIleHisGluAlaThrIleValSerAr 288
      133 GACCGAGATGATCCATGACAGCTC---GGGTACATCAAGKCGCTGTACATATACACCG 77
      288 gProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeuLeuValValValSerAspAs 308
      76 ACCTGTGGCTTCTCTGTGCACAGCGATTAACCTGCTTCTACTCTCTCATCGGTGACAA 17
      308 nPhe 309
      16 GTTC 13

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RESULT 5
CNS04V3 1101 bp DNA linear GSS 24-MAY-2000
LOCUS Tetradon nigroviridis genome survey sequence T3 end of clone
DEFINITION 004B20 of library A from Tetradon nigroviridis, genomic survey
          sequence.
ACCESSION AL309576.1 GI:8216515
VERSION GSS; genome survey sequence.
KEYWORDS Tetradon nigroviridis.
SOURCE Tetradon nigroviridis.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
          Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
          Tetraodontidae; Tetradon.
          1 (bases 1 to 1101)
REFERENCE 1 Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
          Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
          Saurin,W. and Weissenbach,J.
          Human gene number estimate provided by genome wide analysis using
          Tetradon nigroviridis DNA sequence
          Unpublished
          2 (bases 1 to 1101)
REFERENCE 2 Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,
          Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
          Weissenbach,J.
          Characterization and repeat analysis of the compact genome of the
          freshwater pufferfish Tetradon nigroviridis
          Unpublished
          3 (bases 1 to 1101)
REFERENCE 3 Genoscope.
          Direct Submision
          Submitted (12-APR-2000)
          This sequence is a single read and was generated as part of a large
          scale clone-end sequencing project of the Tetradon nigroviridis
          genome. For more information, please take a look at
          http://www.genoscope.cns.fr/Tetradon.
          Location/Qualifiers

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source
1. 1101
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="004B20"
/clone_1fb="A"
/note="Genoscope sequence ID : C0AA004DA10A2-end : T3"
BASE COUNT 225 a 319 c 274 g 274 t 9 others
ORIGIN
Alignment Scores:
Pred. No.: 3.77e-33 Length: 1101
Score: 399.00 Matches: 101
Percent Similarity: 54.21% Conservative: 73
Best Local Similarity: 31.46% Mismatches: 130
Query Match: 22.53% Indels: 17
DB: 17 Gaps: 9
US-10-023-775b-2 (1-337) x CNS04V3 (1-1101)
      23 AsnCysThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyrGlyIle 42
      61 AATGTACAAATAATCNMTGGTTTACTGTGAGAGTACTCTCGCACCTGTGACGGTGTG 120
      43 IlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePheLysMet 62
      121 GAGTTCGCTGGGTGTTTCCCGGACCTGTGTGCTGCTGTTGATATATTTGCTTG 180
      63 ArgProThrLysSerSerThrIleIleMetLeuAsnLeuLysThrAspLeuLeuTyr 82
      181 CCACTGTGGACAGACTCCCATATCTTCACTTCAACCTGGCGCTGACACCTTGTGTTTC 240
      83 LeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyAsnThrIlePheGly 102
      241 CTGTGCACGGTGGCGGACCTCTCTACTGTATACCAACAACAGCTG---CTAAAGAT 297
      103 AspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerIleLeu 122
      298 CCTTCTCTGTGCATCGCCCAACCGGTACATCTGTGACGTCAACCTCTACTCTCATCTC 357
      123 PheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisPheMetSerCysPhe 142
      358 TTTCTGTTGGTGGCTGACATGACCGCTACTCTGTGTGGAGGACCCGACCGGACAC 417
      143 SerIleHisLysThrArgCysAlaValAlaAlaCysAlaValAlaThrIleIleSerLeu 162
      418 TGGCTGTGAMCCGGNCGGCGGCGCTGTGTGACGGGCTGACGCTGTGTGCTGAC 477
      163 ValAlaValIleProMet---ThrPheLeuIleThrSerThrAsnArgThrAsnArgSer 181
      478 GTGGAGGTGGCCCCCATGATAGCGCTGATGTCACAGACCTGCAGAGACACTGAGCA 537
      182 AlaCysLeuAspLeuThrSer---SerAspGluLeuAsnThrIleLysTyrPyrAsnLeu 200
      538 CAGGTAGGACTTCTCCAGCTGTAAGGAGAGCTCAACAGCTTTGTT---TACAGCTTG 594
      201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
      595 GAGCTACACCTGACTGGGTACTCTCGCCCTC-----CTGGCGCTGTGTGGTTTCAC 648
      221 -----IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeu 235
      649 TACCAGATCGCAGCACTGCTCATGTCCAGAGAGAGGCTCTGACGAGGCCACCTCG 708
      236 LysGlnLysAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyrAlaCysPheLeu 255
      709 TTCAAGCGGCCATCGAGGGGTGGCTGAGCTGACGACCATATTTCTCTACACC 768
      256 ProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSerIleSer----- 273
      769 CCACTACCACTGATGAGAACATCAAAATCGCTTACAGAGGTTTGACGAGCTGAT 828
      274 --CysSerIleGluAsnGlnIleHisGluAla-TyrIleValSerArgProLeuAlaI 292

```

[illegible]

QY 232 AspSerCysLeuYsglnAlaArgLeuThrIleLeuLeuAlaPheTyr 251
 Db 600 AACCGAGCAAGAGTCGGCGCTTGTCTGTCGGCGGCTTCGATCTTCATC 659
 QY 252 ValCysPheLeuProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSer 271
 Db 660 GTCTGCTTGGGCCCCAACGCTCTCTCTGAT----- 691
 QY 272 IleSerCysSerIleGluAsnGlnIleHisGlnAlaTyrIleValSerArgProLeuAla 291
 Db 692 -----GTGCATCACTTTCCTCTCTCCGACAGTCTGTGACCA 727
 QY 292 AlaLeuAsnThrPheGlyAsnLeuLeuTyrValValSerAspAsnPheGlnGln 311
 Db 728 GAGCAGCCTACTTGTCTTACTCTCTC----- 754
 QY 312 AlaValCys---SerThrValArgCys 319
 Db 755 TGCCTGTGTGACGACGTGAGCTGC 781

RESULT 9
 BC013202
 LOCUS Homo sapiens, clone IMAGE:4214482, mRNA. Linear HTC 29-AUG-2001
 DEFINITION BC013202.1 GI:15342000
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens.
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2020)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (27-AUG-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT NIH-MGC Project URL: http://mgc.ncl.nih.gov
 Contact: MGC help desk
 Email: gcgaps-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: http://www.hgsc.bcm.tmc.edu/cdna/
 Contact: villalobosbcm.tmc.edu.
 Villalobos, D.K., Luna, R.A., Hale, S.M., Huliyk, S., Lu, X., Garcia,
 A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
 Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://Image.llnl.gov
 Series: IRAC Plate: 26 Row: h Column: 23
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 2695873
 This clone has the following problem: frame shifted.

FEATURES

Source

1..2020
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4214482"
 /tissue_type="Brain, anaplastic oligodendroglioma with
 1p/19q loss"
 /clone_id="NCI_CGAP_Brn67"
 /lab_host="DH10B"
 /note="Vector: PCMV-SPORT6"

BASE COUNT

410 a 689 c 508 g 413 t

ORIGIN

Alignment Scores:
 Pred. No.: 1,35e-29 Length: 2020
 Score: 370.50 Matches: 91
 Percent Similarity: 51.15% Conservative: 65
 Best Local Similarity: 29.84% Mismatches: 136
 Query Match: 20.92% Indels: 14
 DB: 11 Gaps: 6

US-10-023-775B-2 (1-337) x BC013202 (1-2020)

QY 16 AspTyrAlaAlaAlaPheGlyAsnCysThrAspIleuAsnIleProLeuYsMetHisTyr 35
 Db 143 AACTTCTCCCTGGCCAGCAGCAGCAATGTGGCCAGAGACCCACTGGAAACATCTG 202
 QY 36 LeuProValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIle 55
 Db 203 TTGGCCCTCCTTACCTTCCTTGATTTATCTGCTTGTAGTGGCAATACCTGCTG 262
 QY 56 SerThrTyrIlePheLysMetArgProTrrLysSerSerThr-----IleLeuMet 72
 Db 263 TGGCTTTTCATC-----CGAGACCACAAAGTCCGGACCCCGCCAAAGTGTCTG 313
 QY 73 LeuAsnLeuAlaCysThrAspLeuLeuTyrIleuThrSerLeuProPheLeuHisTyr 92
 Db 314 ATGCATCTGGCGCTGGCCGACTGTCTGCTGCTGCTCTCCGCCACCCGCTGTCTAC 373
 QY 93 TyrAlaSerGlyGluAsnTrrIlePheGlyAspPheMetCysLysPheIleArgPheSer 112
 Db 374 CACTTCTCGGAACACACTGGCCCATTTGGGGAATGCCATGCCCTGCACCGCTTCTC 433
 QY 113 PheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyr 132
 Db 434 TTCTACCTCAACAGTACGACGACGACTACTTCTCTCAGCTGCATACAGCGGACCTTC 493
 QY 133 CysValIleIleHisProMetSerCysPheSerIleHisLysThrArgCysAlaValIle 152
 Db 494 CTGGCCATTGTGACCCGGTCAAGTCCCTAAGCTCCGACGCCCCCTTACGCACTTG 553
 QY 153 AlacysAlaValAlaTrrIleIleSerLeuValAlaValIleProMetThrPheLeuIle 172
 Db 554 GCGTGTCTCTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 609
 QY 173 ThrSerThrAsnArgThrAsnArgSer---AlacysLeuAsnLeuThrSerSerPglu 191
 Db 610 CCACAGACCTGTGACAGCAACACACGCTGTCTGCTGCAGCTGTACCGCGAGAGGCC 669
 QY 192 LeuAsnThrIleLysTrrTyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeu 211
 Db 670 TCCAC-----CATGCCCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 717
 QY 212 ValIleValThrLeuCysTrrTrrThrIleIleHisThrLeuThrHisGlyLeuGlnThr 231
 Db 718 ATCACCAGGCTACACTCTACCTGCTGATCATCGGACCTGGCGGAGGCGCTGGGCTG 777
 QY 232 AspSerCysLeuYsglnAlaArgLeuThrIleLeuLeuAlaPheTyr 251
 Db 778 GAGAAAGCGCTCAAGACAGCAGTGCATGTATCCCATATGCGTGGCATCTTCTG 837
 QY 252 ValCysPheLeuProPheHisIleLeuArg---ValIleArgIleGluSerArgLeu 270
 Db 838 GTCTGCTTGGCTTACCTACCTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
 QY 271 SerIleSerCysSerIleGluAsnGlnIleHisGlnAlaTyrIleValSerArgProLeu 290
 Db 898 GGGAGCCTCCTGGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 957
 QY 291 AlaAlaLeuAsnThrPheGlyAsnLeuLeuTyrValValSerAspAsnPheGln 310
 Db 958 ACCAGCCTCAAGCGGACACTGCACCCCATCATGTATTTCTTGTGTGTGAGATTCCG 1017
 QY 311 GlnAlaValCysSer 315
 Db 1018 CACGCCCTGTGCAC 1032

RESULT 10
 AU091121 971 bp mRNA linear EST 23-JAN-2001
 LOCUS AU091121
 DEFINITION AU091121 lambda ZAPR-Con A stimulated leukocytes Paralicthys olivaceus cDNA clone JFCONA882F forward similar to Gallus gallus chemokine receptor-like protein (2412232A), mRNA sequence.
 ACCESSION AU091121
 VERSION AU091121.1 GI:12391161
 KEYWORDS EST
 SOURCE basterd halibut.
 ORGANISM Paralicthys olivaceus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectidae; Paralicthyidae; Paralicthys.
 REFERENCE 1 (bases 1 to 971)
 Nam, B., Hirono, I. and Aoki, T.
 Identification of expressed genes from Japanese flounder (Paralicthys olivaceus) leukocytes stimulated with Con A/PMA
 Unpublished (2000)
 JOURNAL Contact: Ikuro Hirono
 Laboratory of Genetics and Biochemistry
 Tokyo University of Fisheries
 Konan 4-5-7, Minato-ku, Tokyo 108, Japan
 Email: hirono@tokyo-u-fish.ac.jp.
 FEATURES
 source
 1. 971
 /organism="Paralicthys olivaceus"
 /db_xref="taxon:8255"
 /clone="JFCONA882F"
 /clone_1lb="lambda ZAPR-Con A stimulated leukocytes"
 /cell_type="leukocytes"
 /dev_stage="adult"
 /note="common name: Japanese flounder ; injected with peptidoglycan"
 BASE COUNT 205 a 248 c 221 g 297 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 4.91e-30 Length: 971
 Score: 370.00 Matches: 96
 Percent Similarity: 47.66% Conservative: 57
 Best Local Similarity: 29.91% Mismatches: 140
 Query Match: 20.89% Indels: 28
 DB: Gaps: 8
 US-10-023-775b-2 (1-337) x AU091121 (1-971)
 QY 4 ProleuaspTyr-----LeuAlaAsnAlaSerAsp 13
 DB 21 CCGACAGACTACGAGAAATGAGAAATGACACAGACTATGACAAACAGCGTCCGAC 80
 QY 14 PheProaspTyrAlaAlaAlaPheGlyAsnGlyThrAspGlnAsnLeuProleuLys--- 32
 DB 81 CTCGCCAGTCTATATC-----TGTGAGAGAAAGAGAGCGCCCTCCAGACC 125
 QY 33 -----MethisTyrLeuProValIleTyrGlyIleIlePheLeuValGlyPheProGly 50
 DB 126 CTCGGCACTGTTCACGCTGTGTGTACAGCTGATCTTCGCTGGGTGGTGGTGGG 185
 QY 51 AsnAlaValAlaIleSerThrTyrIlePheLysMetArgProTrrpLysSerSerThrIle 70
 DB 186 AACGGCCCTGATGATACAGTCCCTGAGAGCGTTGGCTCCTCGCATCAGATGAGATA 245
 QY 71 IleMetLeuAsnLeuAlaCysThrAspLeuLeuTyrIleThrSerLeuProPheLeuIle 90
 DB 246 TACCTACTTACCTCGCCGCTGCTCATGCTCTTTTAACTCCCTTTCGAGCTG 305
 QY 91 HisTyrTyrAlaSerGlyIleAsnTrrpIlePheGlyAspPheMetCysLysPheIleArg 110
 DB 306 GTCGACTTTCCTCGCTGT-----TGGTGTGGGATTTCTCTCAGACGATGATGGC 359

QY 111 PheSerPheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePhe 130
 DB 360 CTGATGAACATCTCAATCTCCCTGTGGAGTTTCTTTAGCTTCATTTGGTTGAT 419
 QY 131 ArgTyrCysValIleIleHisPrometSerCysPheSerIleHisLysThrArgCysAla 150
 DB 420 CGGATATTGGCTATCGTTCATGGCATTCGCCAGCATGCCAATCGCGCTCCGAGAGCATG 479
 QY 151 ValValAlaCysAlaValAlaTrpIleIleSerLeuAlaValIlePro---MetThr 169
 DB 480 CATGTACTTGTGATTTTACTGTGGCTGTCTGTGGTTATATCAGCTCCAAATTTTGTG 539
 QY 170 PheLeuIleThrSerThrAsnArgThrAsnArgSerAlaCysLeuAspLeuThrSerSer 189
 DB 540 TTTCTTTCTGTGAGAGAGGAGCAACATCAACATCCAGCCTTACTCTCTATATCAT 599
 QY 190 AspGlnLeuAsnThrIleLysTrrpTyr-----AsnLeuIleLeuThrAlaThrPhe 207
 DB 600 CATGACATTCATGACACAACTGGGTTTGTACCAACAGACTTCGATCAGATTTCTTT 659
 QY 208 CysLeuProleuValIleValThrLeuCysTyrThrIleIleHisThrLeuThrHis 227
 DB 660 TTCGTACTCTGTGGCTCATGAGCTACTGCTACACAGAGTGTAGTTACTTGTGTGCAAC 719
 QY 228 GlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArgArgLeuThrIleLeuLeu 247
 DB 720 AGTCAGAAAGCCCAACA-----AACCAAGAGCCATGGAGCTGCTTACTTGTATCAT 773
 QY 248 LeuAlaPheTyrValCysPheLeuProPheHisIleLeuArgValIleArgIleGluSer 267
 DB 774 CTGTCTTTTGGCTCTGTGTGGTCCCATATACATCAGTACTAGATGATGAAACCTGTCA 833
 QY 268 ArgLeuLeuSerIle-----SerCysSerIleLysAsnGlnIleHisGluAlaTyr 284
 DB 834 GACCTGAGAGCTCATCCATGAAAGGTCGCAAACTTTGCTCCCTGCGAGCGCCCTC 893
 QY 285 IleValSerArgProLeuAlaAlaLeuAsnThrPheGlyLysLeuLeuLeuTyrValVal 304
 DB 894 GATGTGTCCCTGAGTCTGGAGATTTCTTACACTGTTCCTGAGAACCCCTTCTTATGCTTC 953
 QY 305 Val 305
 DB 954 ATT 956
 RESULT 11
 AL551903 946 bp mRNA linear EST 16-FEB-2001
 LOCUS AL551903
 DEFINITION AL551903 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1060YJ18 5 prime, mRNA sequence.
 ACCESSION AL551903
 VERSION AL551903.1 GI:12890291
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 946)
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 JOURNAL Contact: Genoscope
 Genoscope Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
 FEATURES
 source
 1. 946
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1060YJ18"
 /clone_1lb="LTI_NFL006.PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com

BASE COUNT 269 a 231 c 168 g 275 t 3 others

Alignment Scores:

Pred. No.: 8 89e-30 Length: 946
Score: 367.50 Matches: 79
Percent Similarity: 49.64% Conservative: 59
Best Local Similarity: 28.42% Mismatches: 123
Query Match: 20.75% Indels: 17
DB: Gaps: 5

US-10-023-775b-2 (1-337) x AL551903 (1-946)

Qy 4 ProleuaspTyrrleuAlaAsnAlaSerAspPhe---ProaspTyrrAlaAlaAlaPheGly 22
Db 55 CCATATGAT---ATACAAATGGCAACAATTTTACTCCGCCCTCTGCACTCCACAGGA 111
Qy 23 AsnCysThrAspGluAsnIleProleuLysMetHisTyr-----Leu 36
Db 112 AATGACTGTGAC-----CTCTATGACATCATCAGACAGCGCCAGATAGTATG 159
Qy 37 ProValIleTyrrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSer 56
Db 160 CCCTGATATACAGCCCTGCTTCATCATTTGGCTGCTGGAACTTACTAGCCCTTGTC 219
Qy 57 ThrTyrrIlePheLysMetArgProTrpLysSerSerThrIleIleMetLeuAsnLeuAla 76
Db 220 GTCATGTTGTAAGAAAGGAAAGAAATCACTACACCTCTATCAACAATTTGTC 279
Qy 77 CysThrAspLeuLeuTyrrIleSerLeuProPheLeuIleHisTyrTyrrAlaSerGly 96
Db 280 AATTTCGATATCTTTTACACCGCTTCTTACACGAAATAGCCCTATGCAATGGC 339
Qy 97 GluAsnTrpIlePheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsn 116
Db 340 TTGGACTGGAGAAATCGGAGATGCTTGTGTAGGATTAACGCGCTAGTGTTTTACATCAAC 399
Qy 117 LeuTyrrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyrrCysValIleIle 136
Db 400 ACATATGACAGTGTGAACCTTTATGACCTGCTGATTTGACCGCTTCATTTGCTGTG 459
Qy 137 HisProMetSerCysPheSerIleHisLysThrArgCysAlaValAlaCysAlaVal 156
Db 460 CACCCTCTACGTCACAAACAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 519
Qy 157 ValTrpIleIleSerLeuValAlaValIlePromethrPheLeuIleThrSerThrAsn 176
Db 520 GTCTGGATTTCTATATTGCTCAGACATCCCACTCTCTATCAACCTTATGCAAGACAG 579
Qy 177 ArgThrAsnArgSerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLys 196
Db 580 GAGCGTAAGAGATTTACATCATGAGATATCCCAACTTTGAAGAAATAATCTCTCCC 639
Qy 197 TrpTyrrAsnLeuIleLeuThrAlaThrPheCysLeuProLeuValIleValThrLeu 216
Db 640 TGGATTCGCTGGGATGTTTCATAGATATGATGCTTCCACTTAAATCATCTGCATC 699
Qy 217 CysTyrrThrThrIleIleHisThrLeu-----ThrHisGlyLeuGlnThr 231
Db 700 TGGTATTTCTAGATGCTGCAAACTCTTCAAGAACTCCCAACAAACCCACTCAGAG 759
Qy 232 AspSerCysLeuLysGlnLysAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyr 251
Db 760 AATCTGCTGTTAACAAGGCTCTCAACACAAATTTCTTATTTGTTGTTGTT 819

Qy 252 ValCysPheLeuProPheHisIleLeuArgValIleArgIleGluSerArgLeu 269
Db 820 CTCTGTTTACACCTTACATGTTGCAWTTATTCACATATAGTAAAGCTT 873

RESULT 12

AL532537

LOCUS 904 bp mRNA linear EST 13-FEB-2001

DEFINITION AL532537 LTI_NFL001_NB04 Homo sapiens cDNA clone CS0DM006Y06 5

ACCESSION AL532537
VERSION AL532537
KEYWORDS prime, mRNA sequence.
SOURCE EST.
human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 904)

AUTHORS Lf.W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France

FEATURES
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.

FEATURES

source

1. 904
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DM006Y06"
/clone_1lb="LTI_NFL001_NB04"
/sex="male"
/tissue="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 260 a 220 c 160 g 264 t

Alignment Scores:

Pred. No.: 1.07e-29 Length: 904
Score: 366.50 Matches: 78
Percent Similarity: 50.00% Conservative: 56
Best Local Similarity: 29.10% Mismatches: 117
Query Match: 20.69% Indels: 17
DB: Gaps: 5

US-10-023-775b-2 (1-337) x AL532537 (1-904)

Qy 4 ProleuaspTyrrleuAlaAsnAlaSerAspPhe---ProaspTyrrAlaAlaAlaPheGly 22
Db 74 CCATATGAT---ATACAAATGGCAACAATTTTACTCCGCCCTCTGCACTCCACAGGA 130
Qy 23 AsnCysThrAspGluAsnIleProleuLysMetHisTyr-----Leu 36
Db 131 AATGACTGTGAC-----CTCTATGACATCATCAGACAGCGCCAGATAGTATG 178
Qy 37 ProValIleTyrrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSer 56
Db 179 CCCTGATTTACAGCCCTGCTTCATCATTTGGCTGCTGGAACTTACTAGCCCTGCTG 238
Qy 57 ThrTyrrIlePheLysMetArgProTrpLysSerSerThrIleIleMetLeuAsnLeuAla 76
Db 239 GTCATTTGTAAGAAAGGAAAGAAATCACTACACCTCTATTCACAAATTTGTC 298
Qy 77 CysThrAspLeuLeuTyrrIleSerLeuProPheLeuIleHisTyrTyrrAlaSerGly 96

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Db      299 ATTTCTGATATCTTTTACACACCGCTTGCCTACACGAAATAGCCCTACTATCATGAGGCG 358
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      359 TTTGACTGGAGATGGAGATGCTGTGTAGGATTAAGTCCCTACTGATCATCAAC 418
      117 LeuYrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIle 136
      419 ACATATGACAGGTGTGACTTATGACTCCCTGAGATGAGCCGCTTCAATGCTGTG 478
      137 HisPrometSerCysPheSerIleHisLysThrArgCysAlaValAlaIleCysAlaVal 156
      479 CACCTCTACGCTACACAAGATMAAAGATTGAACAGCAAAAGCGTGCATATTT 538
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      177 ArgThrAsnArgSerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLys 196
      599 GAGCGTGAAGGATTCATGATGAGATGAGATTCACAACTTGAAGAACTAAATCTTCCC 658
      197 TrpTyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeu 216
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      217 CysTyrThrThrIleIleHisThrLeu-----ThHisLysLeuGlnThr 231
      719 TCTTATTTCTACATCTGCTGCAAACTCTCAGAACTGCCAAACAAACCCACTGCTGAG 778
      232 AspSerCysLeuLysGlnLysAlaArgArgLeuThrIleLeuLeuLeuAlaPheYr 251
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AL547762 LRI_NFL006_PL2 Homo sapiens cDNA clone CSOD1017YN05 5
DEFINITION
prime, mRNA sequence.
ACCESSION
AL547762
VERSION
AL547762.1 GI:12882129
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 931)
L1,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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/db_xref="taxon:9606"
/clone="CSOD1017YN05"
/clone_1lb="LRI_NFL006_PL2"
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/Note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive

```

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : filangeli@fetc.com URL :
<http://fulllength.invitrogen.com>"

BASE COUNT 268 a 224 c 165 g 273 t 1 others

ALIGNMENT Scores:

Pred. No.:	Length:	931
Score:	366.50	78
Percent Similarity:	50.00%	56
Best Local Similarity:	29.10%	117
Query Match:	20.69%	17
DB:	9	5

US-10-023-775b-2 (1-337) x AL547762 (1-931)

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      49  CCAATGATGATATACAAATGCGCAAACTTTTACTCCGCCCTCTGCAACTCCTCAGGGA 105
      23  AsnCysThrAspGluAsnIleProLeuLysMetHisTyr-----Leu 36
      106  AATGACTGTGAC-----CTTATGACATCAGACAGCGCCAGATGATGAAG 153
      37  ProValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSer 56
      154  CCTGTGATATACAGCCTCGCTTCATCATATGGCTGTGGGAACCTTACAGCTTGTC 213
      57  ThrTyrIlePheLysMetArgProTyrLysSerSerThrIleIleMetLeuAsnAla 76
      214  GTCATGTTCAAACAGGAAACAAATCAACTCTACACCCCTCATTCACAAATTTGGTG 273
      77  CysThrAspLeuLeuThrIleThrSerLeuProPheLeuIleHisTyrThrAlaSerGly 96
      274  ATTTCTGATATCTTTTACACACCGCTTGCCTACAGAAATGACCTTATGCAATGGCG 333
      97  GUAsnTrpIlePheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsn 116
      334  TTTGACTGGAGATGGAGATGCTGTGTAGATTAACGCGCTAGTGTTCATCAAC 393
      117  LeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIle 136
      394  ACATATGACAGGTGTGACTTATGACCTCTGAGATTTGACCGCTTCAATGCTGTG 453
      137  HisPrometSerCysPheSerIleHisLysThrArgCysAlaValAlaIleCysAlaVal 156
      454  CACCTCTACGCTACACAAGATMAAAGATTGAACATGCAAAAGCGCTGCTCATATTT 513
      157  ValTrpIleIleSerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsn 176
      514  GTCTGATTTCTAGTATTTGCTGACACCTCCATCATCAACCTTATGTCAAAGCAG 573
      177  ArgThrAsnArgSerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLys 196
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IMAGE:5383884 5', mRNA sequence.
ACCESSION BQ396255
VERSION BQ396255.1 GI:21083932
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 641)
NIH-XGC <http://image.llnl.gov/image/html/xenopuslib.info.shtml>.
National Institute of Child Health and Human Development, National
Cancer Institute, Xenopus Gene Collection
Unpublished (2002)
JOURNAL COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
infoimage.llnl.gov
Plate: L1AM1977 row: N column: 13
Seq primer: M13RPI reverse primer (ABI).
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/tissue_type="neural"
/dev_stage="embryo, stages 14-19"
/lab_host="DH10B (phage-resistant)"
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is a Xenopus Gene Collection (XGC) library."
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Alignment Scores:
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Score: 353.00 Matches: 66
Percent Similarity: 59.66% Conservative: 39
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Query Match: 19.93% Indels: 2
DB: 14 Gaps: 1
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DB 169 GTGGGCTGATCTGTGACATCTGCGCCGTGTACATCTCTGTTCCGGATCAAGCCCTGG 228
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DB 229 AACGCTTCACACACCTACATGTTCAACCTGCGCATTTCCGACATGATGTCATCTCC 288
QY 86 LeuPhePhelelleh1sTyryTyra1aSerGlyGluasnTrp1lePheGlyaspPheMet 105
DB 289 CTCGCCCTGCTGTCTATACCTACGTCAGGGGAGCAACATGCGCTTCGCGCGCTTG 348
QY 106 CysLysPhelellehPheSerPheh1sPheasnLeuTyserSer1leleuPheleuThr 125
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QY 126 CysPheSer1lePhearTyrcysVal1lelleh1sPheMetSerCysPheSer1leH1s 145
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DB 469 AAGCTCGGATGCTCGATATTTCCGTCGTCTGCGGTTCATCTCCGCTTCAG 528
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mRNA sequence.
ACCESSION AL675845
VERSION AL675845.1 GI:19532219
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 638)
Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2002
Unpublished (2001)
JOURNAL COMMENT Contact: Taylor R
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: Tgas051n19, p1cSP6
Sequencing primer: p1cSP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
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into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
BASE COUNT 134 a 180 c 144 g 179 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 2.47e-28 Length: 638
Score: 352.00 Matches: 66
Percent Similarity: 59.66% Conservative: 39
Best Local Similarity: 37.50% Mismatches: 69
Query Match: 19.88% Indels: 2
DB: 9 Gaps: 1
US-10-023-775b-2 (1-337) x AL675845 (1-638)
QY 26 AspGluasn1leProleuysMeth1sTyrlleuProval1leTyg1ylellepheLeu 45
DB 111 GACGAGGAT-----TTCAAGTAGTCCTCTCCGTCGTCGACGATGTCGTCG 164

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: May 29, 2003, 23:41:35 ; Search time 62 Seconds

(without alignments)
1666.937 Million cell updates/sec

Title: US-10-023-775B-2

Perfect score: 1771

Sequence: 1 MNEPLDYLANSDPFDYAA.....RCKVSGNLEQAKKISYNNP 337

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100%
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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5	438	24.7	1842	1	US-08-446-088A-1
6	421	23.8	984	3	US-08-513-974B-41
7	421	23.8	1020	3	US-08-513-974B-370
8	400	22.6	984	3	US-08-513-974B-57
9	400	22.6	1023	3	US-08-513-974B-379
10	394.5	22.3	2577	4	US-09-266-464-1
11	394.5	22.3	1901	1	US-08-153-848-43
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13	394.5	22.3	1901	4	US-09-088-337B-43	Sequence 43, Appl
14	394.5	22.3	1901	5	PCR-US93-11153-43	Sequence 43, Appl
15	394.5	22.3	2453	5	PCR-US95-07180-1	Sequence 1, Appl1
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25	388.5	21.9	3480	1	US-07-789-184-219	Sequence 219, App
26	388.5	21.9	3480	1	US-08-475-263-219	Sequence 219, App
27	388.5	21.9	3480	1	US-08-485-886-219	Sequence 219, App
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34	386.5	21.8	1475	1	US-08-476-000-1	Sequence 1, Appl1
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43	376.5	21.3	1255	1	US-08-476-000-3	Sequence 3, Appl1
44	376.5	21.3	1255	1	US-08-472-840-3	Sequence 3, Appl1
45	376.5	21.3	1255	2	US-08-476-976-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-559-524A-1
; Sequence 1, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-00-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1996 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 625..1626
US-08-559-524A-1

Alignment Scores:
Pred. No.: 3.8e-38
Score: 467.00
Percent Similarity: 55.23%
Best Local Similarity: 35.29%
Query Match: 26.37%
Length: 1996
Matches: 108
Conservative: 61
Mismatch: 125
Indels: 12
Gaps: 6

US-10-023-775B-2 (1-337) x US-08-559-524A-1 (1-1996)

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Db 706 ATTTTATGAGATGAGTTCGTTGAGAGCTCTTGAATACCATGTTGTTTACGGC 765
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QY 158 TyrIleIleSerLeuValAlaValIleProMetThrPheLeuThrIleThrAsnArg 177
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QY 237 ---GlnLysAlaArgArgLeuThrIleLeuLeuLeuValaPheTyrValCysPheLeu 255
Db 1303 CTGGAAGAGCTCTCAACCTTGGTCATCATGAGCAAGGTGATATCTCTCTGCTTTTACA 1362
QY 256 ProPheHisIleLeuArgValIleArgIleGlnSerArgLeuLeuSer-----Ile 272
Db 1363 CCTATCACGCTCATGAGGATGTAGAGATGCTTCAAGCCTGGGAGATTGGAAGCAGATAT 1422
QY 273 SerCysSerIleGlnLysGlnIleHisGlnAlaTyrIleValIleSerArgProLeuAla 292
Db 1423 CAGTGCACCT---CAGGTCGATCATCACTCTTTTACATTTGTGACACGGCTTGGGCTTT 1479

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QY 293 LeuAsnThrPheGlyAsnLeuLeuTyrValValSerAspAsnPheGlnAla 312
Db 1480 CTGAACAGTGCATCAACACCTCTCTCTATTTCTTTGGAGATCACTTACGAGACATG 1539
QY 313 ValCysSerThrValArg 318
Db 1540 CTGATGAATCACTGAGA 1557

RESULT 2
US-08-749-707-1
Sequence 1, Application US/08749707
Patent No. 6063582
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,707
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 044481-5010-01-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1996 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 625..1626
US-08-749-707-1

Alignment Scores:
Pred. No.: 3.8e-38
Score: 467.00
Percent Similarity: 55.23%
Best Local Similarity: 35.29%
Query Match: 26.37%
Length: 1996
Matches: 108
Conservative: 61
Mismatch: 125
Indels: 12
Gaps: 6

US-10-023-775B-2 (1-337) x US-08-749-707-1 (1-1996)

QY 23 AsnCysThrAspGluAsn-----IleProLeuLysMetHisTyrLeuPro 37
Db 646 AATGCAACTGCAAAAACCTGGCTGGCAGACAGAGCTCCCTGGAAGAGTACTACTCTTCC 705
QY 38 ValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThr 57
Db 706 ATTTTATGAGATGAGTTCGTTGAGAGCTCTTGAATACCATGTTGTTTACGGC 765
QY 58 TyrIlePheLysMetArgProTyrPlySerSerThrIleIleMetLeuAsnLeuAlaCys 77

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Db 766 TACATCTCTCTGGAAGACTGGAACAGACGATAATTTATCTTTAACTCTCTGTC 825
Qy 78 ThrAspLeuLeuThyrLeuThrSerLeuProPheLeuIleHisThyTrpTyrIleAspGlyGlu 97
Db 826 TCTGACTTACGCTTTCTTGACACCTCCCTCCATGATGATGAAGAGTATGCCAATGGA--- 882
Qy 98 AsnTrpIlePheGlyAspPheMetCysIlyPheIleArgPheSerPheHisPheAsnLeu 117
Db 883 AACTGATATATGAGACGCTGCTGTCATTAACCAACCGATATGCTTCATGCCAACCTTC 942
Qy 118 TyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHis 137
Db 943 TATACCACTTCTCTTCTTCTTCTTATACACATAGATGATGATGATGATGATGATGATGAT 1002
Qy 138 PrometSerCysPheSerIleHisThyTrpArgCysAlaValAlaValAlaValAlaVal 157
Db 1003 CTTTCCGAGAACACCTTCTGCAAAAGAAAGATTGCTATTTTAATCTCCCTGGCCATT 1062
Qy 158 TrpIleIleSerLeuValAlaValIlePrometThrPheLeuIleThrSerThrAsnArg 177
Db 1063 TGGGTTTAGTAACTTAGACTTAGACTTAGACTTAGACTTAGACTTAGACTTAGACTTAGACT 1122
Qy 178 ThrAsnArgSerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLeuStrp 197
Db 1123 GACAAATGGACACCTGTAATGATTTTGCAGAGTTCGAGACCCCACTACAAACCTCATTT 1182
Qy 198 TyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeuValIleValIleThrLeuCys 217
Db 1183 TACACATGCTGTCTAACACTGTGGGGGCTCTTATTTCTTCTTCTTCTTCTTCTTCTTCTT 1242
Qy 218 TyrThrThrIle---IleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLys 236
Db 1243 TATTACAGATGTGCTCTCTCTCTTAAGCAGAGAAATAGCAGAGTCTCTCTCTCTCTCTCT 1302
Qy 237 ---GlnLysAlaArgArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeu 255
Db 1303 CTTGAAAGCCCTCTCAACTGTGTCATGATGACAGTGTGATCTCTCTCTCTCTCTCTTTTACA 1362
Qy 256 ProPheHisIleLeuArgValIleArgIleGluSerArgLeuLeuSer-----Ile 272
Db 1363 CCGTACACGTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1422
Qy 273 SerCysSerIleGlnAsnGlnIleHisGlnAlaTyrIleValSerArgProLeuAlaIala 292
Db 1423 CAGTGCACT---CAGTGCGTCATCAACCTTTTACATGTGACACGGCCTTTGGCCTTT 1479
Qy 293 LeuAsnThrPheGlyAsnLeuLeuLeuTyrValValValSerAspAsnPhenGlnGlnAla 312
Db 1480 CTGACACAGTGCATGACCCCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1539
Qy 313 ValCysSerThrValArg 318
Db 1540 CTGATGATCACTACAGAGA 1557

RESULT 3
US-08-442-134A-1
; Sequence 1, Application US/08442134A
; Patent No. 5556088
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009

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; CITY: Charlotte
; STATE: No. 5596088th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,134A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ. ID NO. 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..1181
; US-08-442-134A-1

Alignment Scores:
Score: 3,04e-35 Length: 1842
Percent Similarity: 438.00 Matches: 93
Best Local Similarity: 53.908 Conservative: 59
Query Match: 32.988 Mismatches: 118
DB: 24.738 Indels: 12
Gaps: 4

US-10-023-775b-2 (1-337) x US-08-442-134A-1 (1-1842)
Qy 28 AsnIleProLeuIleMetHisThyLeuProValIleTyrGlyIleIlePheLeuValGly 47
Db 138 AACGAGACTTCAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 197
Qy 48 PheProGlyAsnAlaValIleSerThrTyrIlePheLysMetArgProTrpLysSer 67
Db 198 CTGTGCTGACAGCGCTGCGCTCTACATCTTCTTGTGCGCGCTCAAGACCTGAGATGCG 257
Qy 68 SerThrIleIleMetLeuAsnLeuAlaCysThrAspLeuLeuThyrLeuThrSerLeuPro 87
Db 258 TCCACCACTATATATGTTCCACCTGCTGTGTGATGACAGCTATATGCGCGCTGCGCG 317
Qy 88 PheLeuIleHisThyTyrAlaSerGlyGlnAsnTrpIlePheGlyAspPheMetCysLys 107
Db 318 CTGCTGCTTATTTACTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 377
Qy 108 PheIleArgPheSerPheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPhe 127
Db 378 CTGTCGCTGCTCTCTCTTCAACCAACCTTTTACTGACGATCCTCTTCTCACTGACAC 437
Qy 128 SerIlePheArgTyrCysValIleIleHisPrometSerCysPheSerIleHisLysThr 147
Db 438 AGCGTGACACCGGCTGTGCGCGCTTACACCTCTGCGCTGCGCTGCGCGCGCGCGCGCG 497
Qy 148 ArgCysAlaValAlaValAlaCysAlaValAlaValTrpIleSerLeuValAlaValIlePro 167
Db 498 CGTACGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 557
Qy 168 MetThrPheLeuIleThrSerThrAsnArgThrAsnArgSerAlaCysLeuAspLeuThr 187
Db 558 GTGCTCTACTTTGTATCAACACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 614

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DB 906 AACATGCGCTACAGCTTACCCG---CTGGCCAGTGTACAGTTGCCCTTGACCCCGTG 962
OY 301 LeuTyr 302
DB 963 CTCTAC 968

RESULT 5
US-08-446-088A-1
; Sequence 1, Application US/08446088A
; Patent No. 5691156
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691156th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,088A
; FILING DATE: 19-May-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D. Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-861-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..1181
; US-08-446-088A-1

Alignment Scores:
Pred. No.: 3,04e-35 Length: 1842
Score: 438.00 Matches: 93
Percent Similarity: 53.90% Conservative: 59
Best Local Similarity: 32.98% Mismatches: 118
Query Match: 24.73% Indels: 12
DB: 1 Gaps: 4

US-10-023-775B-2 (1-337) x US-08-446-088A-1 (1-1842)
OY 28 AsnIleProLeuLysMetHisTyrLeuProValIleTyrGlyIleIlePheLeuValGly 47
DB 138 AACGAGACTTCAAGTACGTGCTGCTGCTACGCGGTGCTGCTGGG 197
OY 48 PheProGlyAsnAlaValIleSerThrTyrIlePheLysMetArgProTyrLysSer 67

DB 198 CTGTGTCTGAACCGCGTGGCGCTCTACATCTTGTGGCGCTCAAGACCTGGAATGCG 257
OY 68 SerThrIleIleMetLeuAsnLeuAlaCysThrAspLeuLeuTyrIleThrSerLeuPro 87
DB 258 TCCACCAATATATGTTCCACCTGTGTCTGATGACATGTATGCGGCTCGCCG 317
OY 88 PheLeuIleHisTyrTyrAlaSerGlyIleAsnTyrIlePheGlyAspPheMetCysLys 107
DB 318 CTGCTGTCTATATACAGCGCGCGGACCATGTGGCCCTTACAGACAGGCTCTGCAAG 377
OY 108 PheIleArgPheSerPheHisPheAsnLeuTyrSerSerIleLeuPheLeuTyrCysPhe 127
DB 378 CTGCTGCGCTTCTCTTCTACACCACTTACTGACATCTCTTCTCCACCTGCAATC 437
OY 128 SerIlePheArgTyrCysValIleIleHisPheMetSerCysPheSerIleHisLysTyr 147
DB 438 AGCGTGACCGCGTGTGGCGCTTACGACCTGTGCGCTCCCTGCGCGTGGCGCGCC 497
OY 148 ArgCysAlaValAlaValAlaCysAlaValAlaValTyrIleSerLeuValAlaValPro 167
DB 498 CGCTACGCTGCGCGGCGCGCGCGCGCGCTGTGGTGTGGTGGCGCTGCCAGGCCGCC 557
OY 168 MetThrPheLeuIleThrSerThrAsnArgThrAsnArgSerAlaCysLeuAspLeuThr 187
DB 558 GTGCTCTACTTGTACACACACACGCGCGCG---GGCGGCTACCTGCGCACACACTCG 614
OY 188 SerSerAspLeuLeuAsnThrIleLysTyrTyrAsnLeuIleLeuThrAlaThrPhe 207
DB 615 GCACCGGAGCTTTCACCGCGCTGTGGCGCTACAGCTCATGTGTGGCGCTGCTCTTC 674
OY 208 CysLeuProLeuValIleValThrLeuCysTyrThrThrIleIleHisThrLeu----- 225
DB 675 GCGGTGCGCTTGTGCGGTATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 734
OY 226 -----ThrHisGlyLeuGlnThrAspSerCysLeuLysGlnLysAlaArg 240
DB 735 CAGCGTACGCGGAGCGTGGCGCGCTGCTGAG-----GCCAAGCGCAAGTCCGCTG 785
OY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
DB 786 CGCACCATCGCGGTGGCGTGTGCTGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 845
OY 261 ArgValIleArgIleGlyLeuSerArgLeuLeuSerIleSerCysSerIleGlyAsnGlnIle 280
DB 846 CGCACCTCTACTACTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905
OY 281 HisGluAlaTyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeu 300
DB 906 AACATGCGCTACAGGTTACCGG---CTGGCCAGTGTCAAGAGTTCCTGACCCCGTG 962
OY 301 LeuTyr 302
DB 963 CTCTAC 968

RESULT 6
US-08-513-974B-41
; Sequence 41, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston

```

1 STATE: MA
2 COUNTRY: USA
3 ZIP: 02109
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: Patent In Release #1.0, Version #1.30
10
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/08/513,974B
13 FILING DATE: 14-SEP-1995
14 CLASSIFICATION: 536
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: PCT/JP95/01599
17 FILING DATE: 10-AUG-1995
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: JP 7-093989
20 FILING DATE: 19-AUG-1995
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: JP 7-057186
23 FILING DATE: 16-MAR-1995
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: JP 7-007177
26 FILING DATE: 20-JAN-1995
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: JP 6-326611
29 FILING DATE: 28-DEC-1994
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: JP 6-270017
32 FILING DATE: 02-NOV-1994
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: JP 6-236357
35 FILING DATE: 30-SEP-1994
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: JP 6-236356
38 FILING DATE: 30-SEP-1994
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: JP 6-189274
41 FILING DATE: 11-AUG-1994
42 PRIOR APPLICATION DATA:
43 APPLICATION NUMBER: JP 6-189273
44 FILING DATE: 11-AUG-1945
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: JP 6-189272
47 FILING DATE: 11-AUG-1994
48 ATTORNEY/AGENT INFORMATION:
49 NAME: Resnick, David S.
50 REGISTRATION NUMBER: 34,235
51 REFERENCE/DOCKET NUMBER: 45753
52 TELECOMMUNICATION INFORMATION:
53 TELEPHONE: 617-523-3400
54 TELEFAX: 617-523-6440
55 INFORMATION FOR SEQ ID NO: 41:
56 SEQUENCE CHARACTERISTICS:
57 LENGTH: 984 base pairs
58 TYPE: nucleic acid
59 STRANDEDNESS: double
60 TOPOLOGY: linear
61 MOLECULE TYPE: cDNA
62
63 US-08-513-974B-41
64
65 Alignment Scores:
66 Pred. No.: 6,61e-34 Length: 984
67 Score: 421.00 Matches: 96
68 Percent Similarity: 48.29% Conservative: 45
69 Best Local Similarity: 32.88% Mismatches: 125
70 Query Match: 23.77% Indels: 26
71 DB: 3 Gaps: 5
72
73 US-10-023-775B-2 (1-337) x US-08-513-974B-41 (1-984)
74
75 36 LeuProValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValValIle 55
76 ||| ::||| ::::: ::||| ||| |||||

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Db	85	CTAACCCCGGTATACGTGGGGGCGTGGGCGGCGTGCACCTGAAATCTGGGTAT	144
Oy	56	SeThrTyrlIlePheIysMeIarGrProTPrIySerSerThrlIeIleMeIAsnLeu	75
Db	145	GCCAGATCGCCGATCGCCGCGAGCCCGATCGCCGCTGGGTGTACACCCCTGAACCTG	204
Oy	76	AlAcGyThrAspLeuLeuTyrlhrSerIleProPheLeuIleIstTyrlAlaSer	95
Db	205	GCACTGGCGGACCTGATGTATGGCTGTGTACTACCCCTACTATATATACAGCCAGA	264
Oy	96	IlGlyLysAsnTrIlePheGlyAspPheMeIcysIysPheIleArgPheSerIshpe	115
Db	265	GGGACACACGCGCCCTCGGAGACCTCGCGCTCCGCCCTTGTAGCGTCTCTTATGCC	324
Oy	116	AsnLeuTySerSerIleLeuPheLeuThrcysPheSerIlePheArgTyCysValIle	135
Db	325	AACTCATATGGACGATCTCTGTCTCCACCTCATATTACTTCACAGCGCTACCTGGGATC	384
Oy	136	IleIshProMetSerCysPheSerIleIshIys-----ThrArgCysAlaVal	152
Db	385	TGCACCCCTGGCT-----TCCTGGCAAGCTGGAGTGGCGCGCTGTGGTGGTA	438
Oy	153	AlAcCysAlaValAlaTrIleIleSerLeuValAlaValIleProMetThrPheLeuIle	172
Db	439	GTTGTGTGAGATCTGTGGCTGGCTGTGACAGCCCGATGCTGCCACGAGCTTTGCT	498
Oy	173	ThrSerThrAsnArgThrAsnArgSeralAcysIleAspLeuThrSerSerAspIleu	192
Db	499	GCCACAGGATCCAGGCGCAACCGCATGTGTCTACAGACCGACCCACCATCTGTCT	558
Oy	193	AsnThrlIeLysTrpIlyrAsnLeuIleLeuThralaThrlhrPheCysLeuProLeuVal	212
Db	559	ACTGCTACCTGCCCTATGTATGGCCCTACAGGCTACATGGCTTCTTGCCTTCATATA	618
Oy	213	IleValTrIleuCysTyTrThrlhrIleIleIshThrlhrIshIleuGlnThrAsp	232
Db	619	GCTTACTGGCTGTATTATGTGGCATGGCCGCCCGCTG-----	657
Oy	233	SerCys-----LeuIysGlnIysAlaArg	240
Db	658	---TGTCGCGCAGATGGCCACAGGCTCTGTGGCCCAAGAGCGGCGAGCGAGGCT	714
Oy	241	ArgLeuThrlIleLeuLeuLeuAlaPheTyrlValCysPheLeuProPheIshIleu	260
Db	715	CGATGGCTGTGGTGGCGACCTGTCTTGGCATCACACTTCCTGCCTTCACATACCC	774
Oy	261	ArgValIleArgIleGlySerArgLeuLeu---SerIleSerCysSerIleGlyAsnGln	279
Db	775	AAAGACACCTACTGGCTGTGGCTGCACAGCCCGGTGTCTCTTGGCTGTCTGGAAACC	834
Oy	280	IleIshGlyAlaTyrlIleValSerArgProLeuAlaIleAsnThrPheGlyAsnLeu	299
Db	835	TTCGCTGCTGCTACAAAGGACACTCGGCCCTTCGCGAGTGCACAGATGTCTGGACCC	894
Oy	300	LeuLeuTyrlValValValSerAspAsnIleGlnI	311
Db	895	ATTCTCTTACTTTCACACACAGAAATTCGCGCGG	930
RESULT 7			
US-08-513-974B-370			
: Sequence 370, Application US/08513974B			
: Patent No. 6114139			
: GENERAL INFORMATION:			
: APPLICANT: Hisuya, Shuji			
: APPLICANT: Hosoya, Masaki			
: APPLICANT: Fujii, Ryo			
: APPLICANT: Ohtaki, Tetsuya			
: APPLICANT: Fukushima, Shoji			
: APPLICANT: Ohgi, Kazuhiko			
: TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,			
: TITLE OF INVENTION: PRODUCTION, AND USE THEREOF			
: NUMBER OF SEQUENCES: 380			
: CORRESPONDENCE ADDRESS:			

ADDRESSEE: DIKE, BROWNSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
City: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

INFORMATION FOR SEQ. ID NO. 370:
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
type: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:

NAME/KEY: CDS
LOCATION: 28..1011

US-08-513-974B-370

Alignment Scores:	
Pred. No.:	6.97e-34
Score:	421.00
Percent Similarity:	48.29%
Best local Similarity:	32.88%
Query Match:	23.77%
Length:	1020
Matches:	96
Conservative:	45
Mismatches:	125
Indels:	26

[illegible]

APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Ohkaki, Tetsuya
 APPLICANT: Fukusumi, Shoji
 APPLICANT: Ohgi, Kazuhito
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 NUMBER OF SEQUENCES: 380
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/513,974B
 FILING DATE: 14-SEP-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP95/01599
 FILING DATE: 10-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-093989
 FILING DATE: 19-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-057186
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7-007177
 FILING DATE: 20-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-326611
 FILING DATE: 28-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-270017
 FILING DATE: 02-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236357
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-236356
 FILING DATE: 30-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189274
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189273
 FILING DATE: 11-AUG-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 6-189272
 FILING DATE: 11-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Resnick, David S.
 REGISTRATION NUMBER: 34,235
 REFERENCE/DOCKET NUMBER: 45753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 379:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1023 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS

LOCATION: 37..1020
 US-08-513-974B-379
 Alignment Scores:
 Pred. No.: 9,62e-32 Length: 1023
 Score: 400.00 Matches: 93
 Percent Similarity: 47.57% Conservative: 44
 Best Local Similarity: 32.29% Mismatches: 141
 Query Match: 22.59% Indels: 10
 DB: 3 gaps: 4
 US-10-023-775b-2 (1-337) x US-08-513-974B-379 (1-1023)
 QY 32 LysMethisTyrLeuProValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsn 51
 DB 109 AAGCAACTGCTGCTGCGACCTGTGTATGCGCGGTGGCGGCTGGCGCTGCGCTGAC 168
 QY 52 AlalaValIleSerThrTyrIlePheLysMetArgProThrLysSerSerThrIle 71
 DB 169 ATCTGTGCTATTACCGAGATCTGACGCTCCCGCGGCGCTGACCGCGCGCTGTAC 228
 QY 72 MetLeuAsnLeuAlaCysThrAspLeuLeuTyrLeuThrSerLeuProPheLeuIleHis 91
 DB 229 ACCCTAAACCTTCTGCTGCGCTGACCTGTATGCTGCTGCTGCTGCTGCTGCTGCTAC 288
 QY 92 TyrTyrAlaSerGlyGlyAsnTrpIlePheGlyAspPheMetCysLysPheIleArgPhe 111
 DB 289 AACTATGCGCCAGGTGATCACTGCGCCCTTGGCGACTGCTGCGCTGCGCTGCGCTGCTTC 348
 QY 112 SerPheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePheArg 131
 DB 349 CTCTTCTATGCCAACCTGACGCGACGAGATCTCTCTCTACCTGACATCAGTCTGCGCGC 408
 QY 132 TyrCysValIleIleHisProMetSerCysPheSerIleHisLys-----ThrArg 148
 DB 409 TACCTGGGCACTGCGCACCGCGCTGCGCCCTGCG-----CACAAAGTGGGGCGCGCGG 462
 QY 149 CysAlaValAlaValAlaCysAlaValAlaTrpIleIleSerLeuValAlaValIleProMet 168
 DB 463 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 522
 QY 169 ThrPheLeuIleThrSerThrAsnArgThrAsnArgSerAlaCysLeuAspLeuThrSer 188
 DB 523 GCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582
 QY 189 SerAspLeuLeuAsnThrIleLysTrpTyrAsnLeuIleLeuThrAlaThrThrPheCys 208
 DB 583 CTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 642
 QY 209 LeuProLeuValIleValIleThrLeuCysTyrThrIleIleHisThrLeuThrHisGly 228
 DB 643 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702
 QY 229 LeuGlnThrAspSerCysLeuLysGln-----LysAlaArgArgLeuThrIle 244
 DB 703 GATGGCGCGCGCAGAGCGCTGCGCGCAGAGCGCGCGCTGCGCGCGCGCGCGCGCGGTG 762
 QY 245 LeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeuArgValIleArg 264
 DB 763 GTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 822
 QY 265 IleGln---SerArgLeuLeuSerIleSerCysSerIleLeuLysGlnIleHisGlnAla 283
 DB 823 CTGGCAGTGGGCTGCGAGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 882
 QY 284 TyrIleValSerArgProLeuAlaAlaLeuAsnThrPheGlyAsnLeuLeuTyrVal 303
 DB 883 TACAAAGGACAGCGCGCGGTGCGAGTGCACAAAGAGGTGTGTGACCCCAATCTCTGTAC 942
 QY 304 ValValSerAspAsnPheGlnGln 311
 DB 943 TTCACCCAGAAAGATTCCGCGG 966


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;      FEATURE:
;      NAME/KEY: CDS
;      LOCATION: 701..1717
;
US-08-153-848-43

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Alignment Scores:	
Pred. No.:	8,55e-31
Score:	394.50
Percent Similarity:	51.488
Best Local Similarity:	29.888
Query Match:	22,288
DB:	1
	Gaps: 6
	Length: 1901
	Matches: 91
	Conservative: 66
	Mismatches: 135
	Indels: 13
	Gaps: 6

US-10-023-775B-2 (1-337) x US-08-153-848-43 (1-1901)

OY	16	AspTyrAlaAlaPheGlyAsnCySThrAspLysnIleProLeuLysMetHisI	35
		AspTyrAlaAlaPheGlyAsnCySThrAspLysnIleProLeuLysMetHisI	
	740	AACTTCTCCCTGGCCACGACAGCAATGTGGCCAGAGACGCCACTGGAAACATGCTG	799
OY	36	LeuProValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIle	55
		LeuProValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIle	
Db	800	TTGCCTCTCTTACACCTTGTGATTTTATCTGGCTTACTGTGGCAATACCTGGCTG	859
OY	56	SerThrTyrIlePheLysMetArgProTryptylSerSerThr-----IleIleMet	72
		SerThrTyrIlePheLysMetArgProTryptylSerSerThr-----IleIleMet	
Db	860	TGCGTTTTCATC-----CGAGACACAAAGTCGGGAGCCCGGCCAACGTTCCTG	910
OY	73	LeuAsnLeuAlaCysThrAspLeuLeuTyrIleThrSerIleProPheLeuIleHisI	92
		LeuAsnLeuAlaCysThrAspLeuLeuTyrIleThrSerIleProPheLeuIleHisI	
Db	911	ATGCAATGTGGCCCGGCGCCACTTGTCTGGCTGTGGTCTCTGCCACCGCTGTCTAC	970
OY	93	TyrAlaSerGlyIleAsnTrrIlePheGlyAspPheMetCysLysPheIleArgPheSer	112
		TyrAlaSerGlyIleAsnTrrIlePheGlyAspPheMetCysLysPheIleArgPheSer	
Db	971	CACTTCTCTGGGAACCACTGGCCATTTGGGAAATTCGATCGCTCTACCGGCTTCTC	1030
OY	113	PheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyr	132
		PheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyr	
Db	1031	TTCTACTCTCAACATGATACGGCAGCATCTACTTCTCACTCACTCAACGAGCGGCACTTC	1090
OY	133	CysValIleIleHisIlePheMetSerCysPheSerIleHisIleThrArgCysAlaVal	152
		CysValIleIleHisIlePheMetSerCysPheSerIleHisIleThrArgCysAlaVal	
Db	1091	CTGGCCATTGTGGACACCGGTCACGTCCCTCAAGCTCCGGACGCCCTTACGCACACTG	1150
OY	153	AlaCysAlaValAlaTrrIleIleSerLeuValAlaValIleProMetThrPheLeuIle	172
		AlaCysAlaValAlaTrrIleIleSerLeuValAlaValIleProMetThrPheLeuIle	
Db	1151	GGCTGCTCTTCTGTGGT	1207
OY	173	ThrSerThrAsnArgThrAsnArgSer---AlaCysLeuAspLeuThrSerSerAspGlu	191
		ThrSerThrAsnArgThrAsnArgSer---AlaCysLeuAspLeuThrSerSerAspGlu	
Db	1208	CCACAGACCGGTGCAGACCAACACACGCTGTCTGCTGCAGCTGTACCGGAGAAAGCC	1267
OY	192	LeuAsnThrIleLysTrrPyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProleu	211
		LeuAsnThrIleLysTrrPyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProleu	
Db	1268	TCCACAC-----CATGCCCTGTGTCTCCCTGGACAGTGGCCCTTACCTCCGTTTC	1315
OY	212	ValIleValThrLeuCysTyrTrrThrIleIleHisThrLeuThrHisGlyLeuGlnThr	231
		ValIleValThrLeuCysTyrTrrThrIleIleHisThrLeuThrHisGlyLeuGlnThr	
Db	1316	ATCACACAGCGTACACTGTCTACCTGTGATCATTCGCGAAGCGGGCAGGGCTCGTGTG	1375
OY	232	AspSerCysLeuLysGlnIleAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyr	251
		AspSerCysLeuLysGlnIleAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyr	
Db	1376	GAGAAAGCGCTCAAGACCAAGGCGTCCGCTGATTCGCCAATAGTCTGGCCATCTCTCG	1435
OY	252	ValCysPheLeuProPheHisIleLeuArg---ValIleArgIleGluSerArgLeuLeu	270
		ValCysPheLeuProPheHisIleLeuArg---ValIleArgIleGluSerArgLeuLeu	
Db	1436	GTCGTCTTCTGGCTTACACAGTACACCGCTCCGCTTACGCTGTGCACATCCGACCAT	1495
OY	271	SerIleSerCysSerIleGluAsnGlnIleHisGluAlaTyrIleValSerArgProleu	290
		SerIleSerCysSerIleGluAsnGlnIleHisGluAlaTyrIleValSerArgProleu	
Db	1496	GGGCGCTCTGTGGCCACCCACAGCGCATCTGGCCCTGGGAAMACGATACCTCTGCTTC	1555
OY	291	AlaIleLeuAsnThrPheGlyAsnLeuLeuLeuTyrValValValSerAspAsnPheGln	310
		AlaIleLeuAsnThrPheGlyAsnLeuLeuLeuTyrValValValSerAspAsnPheGln	

Db 1556 ACCAGCCCAACGGGGGACACTGGACCCCATGTATTTCCTTCGGCGCTGAGAAAGTCCGC 1615

QY 311 GlnAlaValCysSer 315
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Db 1616 CACGCCCTGTGCAAC 1630

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RESULT 12
US-09-299-843A-43
Sequence 43: Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6500
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 701..1717
US-09-299-843A-43
Alignment Scores:
Pred. No.: 8 55e-31 Length: 1901
Score: 394.50 Matches: 91
Percent Similarity: 51.48% Conservative: 66
Best Local Similarity: 29.84% Mismatches: 135
Query Match: 22.28% Indels: 13
DB: 3 Gaps: 6
US-10-023-775B-2 (1-337) x US-09-299-843A-43 (1-1901)

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DB      740 AACCTCTCCCTGGCCAGCGAGCAATGTGGCCAGAGAGAGCCACATGGAGAACATGCTG 799
      36 LeuProValIleIleTyrglyIleIlePheLeuValIglyPheProglyAsnAlaValIle 55
      800 TTGGCCCTCTTACCTTCTGGATTATCTGCTTTAGTTGGCAATACCTGGCTCTG 859
      56 SerThrTyrIlePheIlePheIleMetArgProTyrPheSerSerThr-----IleIleMet 72
      860 TGGCTTTTCATC-----CGAGACCAACAAGTCCGGAGACCCCGGCAACGTGTCTC 910
      73 LeuAsnLeuAlaCysThrAspLeuLeuTyrLeuThrSerLeuProPheLeuIleHisTyr 92
      911 ATGCATCTGGCCCTGGCCGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAC 970
      93 TyrAlaSerGlyIleAsnTrpIlePheGlyAspPheMetCysIlePheIleArgPheSer 112
      971 CACTTCTCTGGAGAACCACTGGCCATTTGGGGAAATCGCATGCCGTCTACCGGCTTCTC 1030
      113 PheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyr 132
      1031 TTCTACCTCAACATGATGAGCCAGCATCTACTCTCTCATCTGATCAGATCAGCCGAGCCGTTTC 1090
      133 CysValIleIleIleHisProMetSerCysPheSerIleHisIleThrArgCysAlaValVal 152
      1091 CTGGCCATGTGGACCCGCGCAAGTCCCTCAAGCTCCGAGGAGCCCTCTACGACACACCTG 1150
      153 AlaCysAlaValAlaValTrpIleIleSerLeuValAlaValIleProMetThrPheLeuIle 172
      1151 GCCTGTGCTCTCTGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 1207
      173 ThrSerThrAsnArgThrAsnArgSer--AlaCysLeuAspLeuThrSerSerAspGlu 191
      1208 CCACAGACCGTGCAGACCAACACACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1267
      192 LeuAsnThrIleLeuTyrTrpIleAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeu 211
      1268 TCCACAC-----CATGCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1315
      212 ValIleValThrLeuCysTyrThrThrIleIleHisThrLeuThrHisGlyLeuAsnThr 231
      1316 ATACACACGCTACCTGCTACCTGCTACCTGCTACCTGCTACCTGCTGCGGAGCGGCTGCGGTG 1375
      232 AspSerCysLeuIleGlyAsnAlaArgArgLeuThrIleLeuLeuLeuAlaPheTyr 251
      1376 GAGAACGCGCTCAAGACCAAGCATGTCGATGATGCGCATGATGCGCATGATGCGCATGCTTC 1435
      252 ValCysPheLeuProPheHisIleLeuArg--ValIleArgIleGlyLeuSerArgLeu 270
      1436 GTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1495
      271 SerIleSerCysSerIleGluAsnGlnIleHisGlnAlaTyrIleValSerArgProLeu 290
      1496 GGGGCTCTGCTGGCCAGCCAGCATCTGCGCTGCGCAACGCGCATCTGCTGCTGCTGCTGCTG 1555
      291 AlaAlaLeuAsnThrPheGlyAsnLeuLeuTyrValValValSerAspAsnPheGln 310
      1556 ACCAGGCTCAACGCGGACACTGACACCATCATATTTCTTCTGCTGAGATGCTCCG 1615
      311 GlnAlaValCysSer 315
      1616 CACGCCCTGTGCAC 1630

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RESULT 13
US-09-088-337B-43

; Sequence 43, Application US/09088337B
; Patent No. 6348574

; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald

; Gray, Patrick W.

; Schwellkart, Vicki L.

; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
            Borun
            STREET: 6300 Sears Tower, 233 South Wacker Drive
            CITY: Chicago
            STATE: Illinois
            COUNTRY: USA
            ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 701..1717
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-088-337B-43
Alignment Scores:
Pred. No.: 8,55e-31 Length: 1901
Score: 394.50 Matches: 91
Percent Similarity: 51.48% Conservative: 66
Best Local Similarity: 29.84% Mismatches: 135
Query Match: 22.28% Indels: 13
Gaps: 6
US-10-023-775B-2 (1-337) x US-09-088-337B-43 (1-1901)
      16 AspTyrAlaAlaIlePheGlyAsnCysThrAspGluAsnIleProLeuIleMethIleTyr 35
      740 AACCTCTCCCTGGCCAGCGAGCAATGTGGCCAGAGAGAGCCACATGGAGAACATGCTG 799
      36 LeuProValIleIleTyrglyIleIlePheLeuValIglyPheProglyAsnAlaValIle 55
      800 TTGGCCCTCTTACCTTCTGGATTATCTGCTTTAGTTGGCAATACCTGGCTCTG 859
      56 SerThrTyrIlePheIlePheIleMetArgProTyrPheSerSerThr-----IleIleMet 72
      860 TGGCTTTTCATC-----CGAGACCAACAAGTCCGGAGACCCCGGCAACGTGTCTC 910
      73 LeuAsnLeuAlaCysThrAspLeuLeuTyrLeuThrSerLeuProPheLeuIleHisTyr 92
      911 ATGCATCTGGCCCTGGCCGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAC 970
      93 TyrAlaSerGlyIleAsnTrpIlePheGlyAspPheMetCysIlePheIleArgPheSer 112
      971 CACTTCTCTGGAGAACCACTGGCCATTTGGGGAAATCGCATGCCGTCTACCGGCTTCTC 1030

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QY 113 pheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyr 132
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1031 TTCTACCTCAACATGATGACCGACGACATCTACTCTACCTGATGACGCGGACCGCTTTC 1090
QY 133 CysValIleIleHisProMetSerCysPheSerIleHisIleThrArgCysAlaVal 152
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1091 CTGGCCATTGTGCACCGCGTCAAGTCCCTCAAGCTCCGACGCGCCCTTACCCACACCTG 1150
QY 153 AlaCysAlaValAlaValIleIleSerLeuValAlaValIleProMetThrPheLeuIle 172
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1151 GCGTGCCTCTCTCCGTGGGTGGTGGTGGCTGGCGCTGCGCCGCTG---CTGGAGAC 1207
QY 173 ThrSerThrAsnArgThrAsnArgSer---AlaCysLeuAspLeuThrSerSerArgIu 191
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1208 CCACAGACCGGTGACAGACCAACACACGAGTGGTGGCTGCTGACCTGACCGGAGAGAGGCC 1267
QY 192 LeuAsnThrIleIleTyrTrpTyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeu 211
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1268 TCCAC---CATGCGCTGGTGTCCCTGGCAGTGGCGCTTACCTTCCCGTTC 1315
QY 212 ValIleValThrLeuCysTyrThrThrIleIleHisThrLeuThrHisIleuGlnThr 231
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1316 ATCACCACGGTACCGCTACCTGCTGATCATCCGACGCTGCGGAGGCGCTGGTG 1375
QY 232 AspSerCysLeuIleGlnIleValArgAlaArgLeuThrIleLeuLeuLeuAlaPheTyr 251
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1376 GAGACGCGCTCAAGACCAAGCAGCGCATGCGCATGCGCATGCTGGCCATCTTCCG 1435
QY 252 ValCysPheLeuProPheHisIleLeuArg---ValIleArgIleGlnSerArgLeuLeu 270
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1436 GTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1495
QY 271 SerIleSerCysSerIleGlnGlnGlnIleHisGlnAlaTyrIleValSerArgProLeu 290
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1496 GGGGCTCTCTGCGCCACCGACGCGCATCTGGCGCTGGACACCGCATCTCTGCTGCTG 1555
QY 291 AlaAlaLeuAsnThrPheGlyAsnLeuLeuLeuTyrValValSerAspAsnPheGln 310
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1556 ACCAGCTCAACGGGCGACTCGACCCCATCATGATTTCTGCTGCTGAGAAAGTTCCG 1615
QY 311 GlnAlaValCysSer 315
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1616 CACGCCCTGTGCAAC 1630

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RESULT 14
PCT-US93-11153-43
; Sequence 43, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schwellhart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992

```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1901 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 701..1717
; PCT-US93-11153-43
;
; Alignment Scores:
; Pred. No.: 8,55e-31 Length: 1901
; Score: 394.50 Matches: 91
; Percent Similarity: 51.48% Conservative: 66
; Best Local Similarity: 29.84% Mismatches: 135
; Query Match: 22.28% Indels: 13
; DB: 5 Gaps: 6
;
; US-10-023-775b-2 (1-337) x PCT-US93-11153-43 (1-1901)
;
QY 16 AspTyrAlaAlaAlaPheGlyAsnCysThrAspGluAsnIleProLeuIleMetHisTyr 35
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 740 AACTTCTCTCGGCGCGGACGACGACATGTGGCGGAGACCGGACGACGACGACGACGACG 799
QY 36 LeuProValIleIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIle 55
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 800 TTGCGCTCTCTGACCTTGTGATTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
QY 56 SerThrTyrIlePheIleMetArgProTyrPheSerSerThr-----IleIleMet 72
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 860 TGGCTTTTCATC-----CGAGACCAAGTCCGGAGACCCCGGACCAAGCTGTCG 910
QY 73 LeuAsnLeuAlaCysThrAspLeuLeuTyrIleThrSerLeuProPheLeuIleHisTyr 92
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 911 ATGCATCTGCGCGTGGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 970
QY 93 TyrAlaSerGlyGlnAsnThrIlePheGlyAspPheMetCysLysPheIleArgPheSer 112
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 971 CACTTCTCTGGGACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1030
QY 113 PheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyr 132
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1031 TTCTACCTCAACATGATGACCGACGACATCTACTCTACCTGATGACGCGGACCGCTTTC 1090
QY 133 CysValIleIleHisProMetSerCysPheSerIleHisIleThrArgCysAlaVal 152
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1091 CTGGCCATTGTGCACCGCGTCAAGTCCCTCAAGCTCCGACGCGCCCTTACCCACACCTG 1150
QY 153 AlaCysAlaValAlaValIleIleSerLeuValAlaValIleProMetThrPheLeuIle 172
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1151 GCGTGCCTCTCTCCGTGGGTGGTGGTGGCTGGCGCTGCGCCGCTG---CTGGAGAC 1207
QY 173 ThrSerThrAsnArgThrAsnArgSer---AlaCysLeuAspLeuThrSerSerArgIu 191
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1208 CCACAGACCGGTGACAGACCAACACACGAGTGGTGGCTGCTGACCTGACCGGAGAGAGGCC 1267
QY 192 LeuAsnThrIleIleTyrTrpTyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeu 211
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1268 TCCAC---CATGCGCTGGTGTCCCTGGCAGTGGCGCTTACCTTCCCGTTC 1315
QY 212 ValIleValThrLeuCysTyrThrThrIleIleHisThrLeuThrHisIleuGlnThr 231
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Db 1316 ATCACCACGGTACCGCTACCTGCTGATCATCCGACGCTGCGGAGGCGCTGGTG 1375

```

QY 232 AspSerCysLeuYsglnLysAlaArgLeuThrIleLeuLeuLeuAlaPheTyr 251
 Db 1376 GAGAGCGGCTCAAGACGACGAGCATGATGCGCATGATGCGCATCTTCCTG 1435
 QY 252 ValCysPheLeuProPheHisIleLeuArg---ValIleArgIleGlnSerArgLeu 270
 Db 1436 GTCTGCTGCTGCGCTACGACGTCACCGCTCGCTACGCTGACCTACCGACCAT 1495
 QY 271 SerIleSerCysSerIleGlnAsnGlnIleHisGlnAlaTyrIleValSerArgProLeu 290
 Db 1496 GGGGCGCTCGCGCACCACCGCATCTGCGCTGCGCAACCGCATCCTCTGCTC 1555
 QY 291 AlaAlaLeuAsnThrPheGlyAsnLeuLeuTyrValValSerAspAsnPheGln 310
 Db 1556 ACCAGCCTCAACGGGCGCATCTGACCCCATCATGATTTCTTCGCTGAGAACTTCGCG 1615
 QY 311 GlnAlaValCysSer 315
 Db 1616 CACGCCCTGTGCAC 1630

RESULT 15 PCT-US95-07180-1

Sequence 1, Application PC/TUS9507180
GENERAL INFORMATION:

APPLICANT: LI, YI
 APPLICANT: GOCAYNE, JEANINE D
 APPLICANT: RUBEN, STEVEN M
 TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ADDRESSEE: STEWART & OLSTEIN
 STREET: 6 BECKER FARM ROAD
 CITY: ROSELAND
 STATE: NJ
 COUNTRY: US

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07180

FILING DATE: 06-JUNE-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 30,073

REFERENCE/DOCKET NUMBER: 325800-366

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1740

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2453 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 548..1564

PCT-US95-07180-1

Alignment Scores:

Pred. No.: 1.24e-30 Length: 2453
 Score: 394.50 Matches: 91
 Percent Similarity: 51.48% Conservative: 66
 Best Local Similarity: 29.84% Mismatches: 135
 Query Match: 22.28% Indels: 13
 DB: 5 Gaps: 6

US-10-023-775b-2 (1-337) x PCT-US95-07180-1 (1-2453)
 QY 16 AspTyrAlaIleAlaPheGlyAsnCysThrAspGlnAsnIleProLeuYsMetHisTyr 35
 Db 587 AACTTCTCCCTGGCCACGACGACGAAATGTGGCCAGACAGCCACTGGAGAAATCTCTG 646
 QY 36 LeuProValIleTyrGlyIleIlePheLeuValGlyPheProGlyAsnAlaValIle 55
 Db 647 TTGCGCTCTTACCTTCTGATTTATCTGCTGCTTACTGTGCAATACCTGCGCTCTG 706
 QY 56 SerThrTyrIlePheIleYsMetArgProTyrPysSerThr-----IleIleMet 72
 Db 707 TGGCTTTTCATC-----CGAGACCAACAGTCCGGGACCCCGGCAAGTTCCTG 757
 QY 73 LeuAsnLeuIleCysThrAspLeuTyrLeuThrSerLeuProPheIleHisTyr 92
 Db 758 ATGCATCTGGCCGCGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 817
 QY 93 TyrAlaSerGlyGlnAsnTyrIlePheGlyAspPheMetCysIlePheIleArgPheSer 112
 Db 818 CACTTCTCTGGAAACACATGCGCATTTGGGAAATCGACCGCTCACCGGCTTCCTC 877
 QY 113 PheHisPheAsnLeuTyrSerSerIleLeuPheLeuThrCysPheSerIlePheArgTyr 132
 Db 878 TTCTACCTCAACATGACGACCATCTACTTCTCTCACTGACATCAGCCGACCGCTTC 937
 QY 133 CysValIleIleIleHisProMetSerCysPheSerIleHisTyrThrArgCysAlaVal 152
 Db 938 CTGGCCATTGTGACACCGCGTCAGTCCCTCAAGCTCCGACGCGCCCTCAAGCAGCTG 997
 QY 153 AlaCysAlaValValTyrIleIleSerLeuValAlaValIleProMetThrPheLeuIle 172
 Db 998 GCCTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054
 QY 173 ThrSerThrAsnArgThrAsnArgSer---AlaCysLeuAsnPyrThrSerAspGln 191
 Db 1055 CCACAGACGCTGACGACCAACACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1114
 QY 192 LeuAsnThrIleIleTyrTyrAsnLeuIleLeuThrAlaThrThrPheCysLeuProLeu 211
 Db 1115 TCCGAC-----CATGCCCTGGTCTCCCTGCACTGACCTTACCTTCCGCTTC 1162
 QY 212 ValIleValThrLeuCysTyrThrThrIleIleHisThrLeuThrHisGlyLeuGlnThr 231
 Db 1163 ATCACACGCTCACCTGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1222
 QY 232 AspSerCysLeuYsglnLysAlaArgLeuThrIleLeuLeuLeuAlaPheTyr 251
 Db 1223 GAGAGCGGCTCAAGACGACGAGCATGATGCGCATGATGCGCATCTTCCTG 1282
 QY 252 ValCysPheLeuProPheHisIleLeuArg---ValIleArgIleGlnSerArgLeu 270
 Db 1283 GTCTGCTGCTGCGCTACGACGTCACCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1342
 QY 271 SerIleSerCysSerIleGlnAsnGlnIleHisGlnAlaTyrIleValSerArgProLeu 290
 Db 1343 GGGGCGCTCGCGCACCACCGCATCTGCGCTGCGCAACCGCATCCTCTGCTC 1402
 QY 291 AlaAlaLeuAsnThrPheGlyAsnLeuLeuTyrValValSerAspAsnPheGln 310
 Db 1403 ACCAGCCTCAACGGGCGCATCTGACCCCATCATGATTTCTTCGCTGAGAACTTCGCG 1462
 QY 311 GlnAlaValCysSer 315
 Db 1463 CACGCCCTGTGCAC 1477

Search completed: May 30, 2003, 01:12:39
Job time: 70 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2003, 22:13:19 ; Search time 1746 Seconds

(without alignments)
9405.626 Million cell updates/sec

Title: US-10-023-775b-1

Perfect score: 1014
Sequence: 1 atgaatgagccactagacta.....gttactcaaacaccttga 1014

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estlro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_trod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	243	24.0	744	14	BM723768 UI-E-EOI-
2	126.6	12.5	623	14	B0038875 pgnlc.pk0
3	115.8	11.4	641	14	B0396255 NISC-ng19
4	114.8	11.3	638	9	AL675845
5	109.4	10.8	877	12	BG402029 602466748
6	108.8	10.7	663	13	BM426517 pgf2n.pk0

C	7	107.4	10.6	1101	17	CNS05325	AL318925 Tetradon
	8	106.2	10.5	491	12	BG712193	BG712193 pgnlc.pk0
	9	103	10.2	609	9	AL588350	AL588350 AL588350
	10	102	10.1	520	9	AL663305	AL663305 UK27c10.y
	11	100.4	9.9	2542	11	AK017378	AK017378 Mus muscu
	12	100.4	9.9	3001	11	AK005013	AK005013 Mus muscu
	13	100	9.8	422	10	BB847918	BB847918 BB847918
	14	99.6	9.8	801	13	BG924078	BG924078 602823635
	15	98.4	9.7	606	17	B4293874	B4293874 2M0219117
	16	95.8	9.4	408	13	B1401676	B1401676 MT-P-CPD-
	17	95.6	9.4	851	13	B1833118	B1833118 603090834
	18	94.2	9.3	1063	14	BM918491	BM918491 AGENCOURT
	19	94	9.3	420	10	BB864882	BB864882 BB864882
	20	94	9.3	884	9	AL525099	AL525099 AL525099
	21	94	9.3	898	13	B1819396	B1819396 603034571
	22	94	9.3	936	9	AL520218	AL520218 AL520218
	23	93.8	9.3	484	14	B0551383	B0551383 H4008H11-
	24	93.8	9.3	523	9	AL836006	AL836006 AL836006
	25	93.8	9.3	839	14	B0897419	B0897419 AGENCOURT
	26	93.6	9.2	955	9	AL521440	AL521440 AL521440
	27	93.4	9.2	934	13	B1768397	B1768397 603053844
	28	92.6	9.1	983	17	CNS043P5	AL775666 Tetradon
C	29	92.4	9.1	899	14	BQ959110	BQ959110 AGENCOURT
	30	91.6	9.0	678	10	BE314834	BE314834 601147561
	31	89.8	8.9	589	14	BQ396804	BQ396804 NISC-ng23
	32	89.4	8.8	581	13	BM258063	BM258063 522739.MA
	33	87.6	8.6	752	13	BM008116	BM008116 603618002
	34	87.6	8.6	801	13	B1837965	B1837965 603083801
	35	87.6	8.6	870	9	AL545172	AL545172 AL545172
	36	87.6	8.6	885	9	AL546894	AL546894 AL546894
	37	87.6	8.6	1057	14	BM918711	BM918711 AGENCOURT
	38	87.6	8.6	2146	11	BC027965	BC027965 Homo sapi
	39	87.2	8.6	529	9	AA177828	AA177828 mt07f02.f
	40	87.2	8.6	585	10	BE627479	BE627479 uu52b07.y
	41	86.8	8.6	570	12	BG579061	BG579061 df22e05.y
	42	86.8	8.6	869	14	BQ724793	BQ724793 AGENCOURT
	43	86.6	8.5	516	9	AL698846	AL698846 DKFZP686P
	44	86	8.5	734	13	BG914321	BG914321 602810633
	45	86	8.5	1082	14	BQ710754	BQ710754 AGENCOURT

ALIGNMENTS

RESULT 1
BM723768
LOCUS 744 bp mRNA linear EST 01-MAR-2002
DEFINITION UI-E-EOI-aiix-g-16-0-UI.r1 UI-E-EOI Homo sapiens cDNA clone
ACCESSION BM723768
VERSION UI-E-EOI-aiix-g-16-0-UI 5', mRNA sequence.
KEYWORDS BM723768.1 GI:19045099
EST.

SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 744)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996).

JOURNAL

MEDLINE 97044477
COMMENT

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers

FEATURES

source

1. 744

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-E-EO1-16-0-01"

/clone_11d="UI-E-EO1"

/tissue_type="fetal eye"

/dev_stage="fetal"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/note="Organ: eye; Vector: pRT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-EO1 is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldi, Lennon and Seares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the Program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 217 a 168 c 126 g 233 t

ORIGIN

Query Match 24.0%; Score 243; DB 14; Length 744;

Best Local Similarity 100.0%; Pred. No. 3.4e-60;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

772 CATATCTGAGGCGATTCGATCGATGATCGCTGCTTCAACATGTTGTCATGAG 831
1 CATATCTGAGGCGATTCGATCGATGATCGCTGCTTCAACATGTTGTCATGAG 60
832 AATCAGATCCATGAGCTTACATCGTTTCTAGACATTAGCTGCTGAACACCTTGGT 891
61 AATCAGATCCATGAGCTTACATCGTTTCTAGACATTAGCTGCTGAACACCTTGGT 120
892 AACCTGTTACTATATGTTGTTGTCAGGACACTTTCAGAGGCTGCTGCTCAACAGTG 951
121 AACCTGTTACTATATGTTGTTGTCAGGACACTTTCAGAGGCTGCTGCTCAACAGTG 180
952 AGATGCAAAATAGCGGAGACCTTGAGCAAGCAAAATAGTACTCAACACCTT 1011
181 AGATGCAAAATAGCGGAGACCTTGAGCAAGCAAAATAGTACTCAACACCTT 240
1012 TGA 1014
241 TGA 243

RESULT 2
LOCUS B0038875
DEFINITION B0038875 623 bp. mRNA linear. EST 01-MAY-2002
gnic.pk010.113 normalized chicken lymphoid cDNA library Gallus
gallus cDNA clone gnic.pk010.113 5' similar to
SP1P34996|P2YR.CHICK P2Y PURINORECEPTOR 1 (P2Y1)
(PURINERGIC RECEPTOR) PIR|S33733 G protein-coupled receptor -
chicken emb|CA51716.1| (X73268) ATP receptor P2Y1 [Gallus gallus],
mRNA sequence.

ACCESSION B0038875
VERSION B0038875.2 GI:20383637
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.

REFERENCE 1. (bases 1 to 623)
AUTHORS Morgan, R.W. and Burnside, J.
TITLE Chicken Lymphoid ESTs
JOURNAL Unpublished (2001)
COMMENT On Mar 27, 2002 this sequence version replaced gi:19772415.

Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302 831-3411
Email: joan@udel.edu, www.chickest.udel.edu.

FEATURES

source

1. 623

/organism="Gallus gallus"

/db_xref="taxon:9031"

/clone="gnic.pk010.113"

/clone_11d="normalized chicken lymphoid cDNA library"

/sex="Male and Female"

/tissue_type="thymus, bursa, spleen, PBL, bone marrow"

/lab_host="E. coli EMDH10B"

/note="Vector: pCMVSPORT 6"

BASE COUNT 117 a 199 c 172 g 128 t 7 others

ORIGIN

Query Match 12.5%; Score 126.6; DB 14; Length 623;

Best Local Similarity 53.6%; Pred. No. 5.8e-26;

Matches 258; Conservative 0; Mismatches 223; Indels 0; Gaps 0;

92 TCAGATGACACTTCTCCCTGTTATATGATATATCTTCCTGCGGATTTCCAGCA 151
124 TCAGATGACACTTCTCCCTGTTATATGATATATCTTCCTGCGGATTTCCAGCA 183
152 ATGACATGATGATATATGATATATGATATATGATATATGATATATGATATATG 211
184 ACAGCGTGGCATCTGATGTTGCTCTTCACATGCGGCGGTGAGGCGATCTGGTGT 243
212 TTATGCTGAACCTGCGCTGACAGATCTGCTATCTGACAGACCTCCCTGATTC 271
244 ACATGTTCAACCTGCGCTGCGGACATCTGATATGCTGACAGCTCCGCGCTATCT 303
272 ACTATGATGACAGCTGCGGAGAACTGATCTTTGAGATTTCAATGATATATGCT 331
304 TCTACTACTTCAACAAACACCGATGATCTTCTGCGGAGCTGATGATGATGATG 363
332 TCAGCTTCAATTCACCTGATATAGCAGATCTCTCTCACCTGTTTACGATCTCC 391
364 TCAATTTTCCACGTAACCTTACGCGACGATCTCTCTCACGTCATTAAGCTGCACA 423
392 GCTACTGTGATCATTCACCAATGAGCTGTTTCCATTCACAAACTGATGTGACG 451
424 GGTACAGGCGGCTGCTGACACCGCTGAAATGCGTGGGAGCTGAAAGAAACAGCG 483
452 TTGAGCCTGTGCTGTGATGATATCTTCACTGATGATGATGATGATGATGATG 511
484 TGTACGTCACTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
512 TGATCATCATCAACCAACAGCAACAGATGATGATGATGATGATGATGATGATG 571
544 ACTCAGGAGCAGNNNGAGAGAGAAACCAATCAGTGTCTTACGACACACGCGNAG 603
572 A 572
604 A 604

RESULT 3
LOCUS B0396255
DEFINITION B0396255 641 bp. mRNA linear. EST 22-MAY-2002
NISC.n919g07.y1 NICHHD XGC Emb6 Silurana tropicalis cDNA clone
IMAGE:5383864 5', mRNA sequence.
ACCESSION B0396255
VERSION B0396255.1 GI:21083932

Oy		572	AACCTAPACTATTAGGCGAACCACTAAT	602
Dd		605	TATTGACAACCTTGCTGTACGACACAGT	635
<hr/>				
RESULT 4				
LOCUS	AL675845	638 bp	mRNA	linear EST 18-MAR-2002
DEFINITION	AL675845 XGC-gastrula Silurana tropicalis cDNA clone Tgas05in19 5'			
ACCESSION	AL675845			
VERSION	AL675845.1	GI:19532219		
KEYWORDS	EST.			
SOURCE	western clawed frog.			
ORGANISM	Silurana tropicalis			
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Piplidae;			
	Xenopodinae; Silurana.			
	1 (bases 1 to 638)			
REFERENCE	Taylor,R., Ashurst,J.L., Croning,M.D.R., Zorn,A.M. and Rogers,J.			
AUTHORS	Sanger Xenopus tropicalis EST project 2002			
TITLE	Unpublished (2001)			
JOURNAL	Contact: Taylor R			
COMMENT	Sanger Centre Hinxton, Cambridgeshire, CB10 1SA, UK Email: tropesanger.ac.uk Sanger Xenopus tropicalis EST project 2001 TROPOCALIS_SEQUENCE_ID: Tgas05in19.picsP6 Sequencing primer: PICSP6 This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn. Location/Qualifiers 1..638 /organism="Silurana tropicalis" /db_xref="taxon:8364" /clone="Tgas05in19" /clone_lib="gsc-gastrula" /dev_stage="gastrula (stages 10.5-13 mixed)" /lab_host="Escherichia coli XL1-blue" /note="Vector: PCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into PCS107 with EcoRI at the 5' end and NotI at the 3' end."			
FEATURES				
SOURCE				
BASE COUNT	134 a	180 c	144 g	179 t
ORIGIN				1 others
Query Match	11.3%; Score 114.8; DB 9; Length 638;			
Best Local Similarity	51.5%; Pred. No. 1.7e-22;			
Matches	263; Conservative	0; Mismatches	248; Indels	0; Gaps
Oy	92	TCAGAGTGCACACTCCCTCCTTTATTTATGACATTAATCTCCCTGGGATTTCCAGCA	151	
Dd	121	TCAAGTAGCTCCTCCTCCCCCGTGCATGCGGACATCGTGTGCGTGCGGCTGATCCGA	180	
Oy	152	ATGCAAGTAGATATATCCACTACATTTCAAATGAAAGAGCTTGGAAAGAGCACACATCA	211	
Dd	181	ACATTTGGCCCTGACATCTTCTCTGTTCCGATCAAGCCCTGGAAACCCTTCACCACT	240	
Oy	212	TTATGCTGAACCTTGCGCTGCAGATCTGCTATCTGACCAAGCCTCCCTTCCTGATTC	271	
Dd	241	ACATGTTCAACCTGGCCATTTCCGACATGATGATGATGATGCCCTCCGGTGGCGGCT	300	
Oy	272	ACTACATGACGAGTGGCGAAAACATGATCTTTGGAGATTTATGTGTAAGTTATCCGCT	331	
Dd	301	ATTACTATCCACAGGGGACAAACATGCGCGTTCGGCGCTTGCGAAGATCGCAAGT	360	
Oy	332	TCAGCTTCATTTCAACCTGATATGACACATCTTCCTCAACCGTGTTCAGCATCTCC	391	
Dd	361	TCCTTTTCTACACCAACATGTACGTACATCTCTCTTCTGTGATCAGCATCACC	420	
Oy	392	GCTACGTGTGATCAATTCACCAATGAGCTGCTTTTCCATTACAAAACTGATGTGCG	451	

Db	421	GCTTCCTGGGATCTGCTACCCAAATGAATCACTGGCTGGTGAAGTGGCAATGCTC	480
QY	452	TTTGAACCTGTGCTGTGTGTGATCATTTACGTAGTCACTTCATTCOGATGACCTCT	511
Db	481	GGATTATTTCCGTGGTGGCTGGGTTATGCTTTCCGCTGTCAGTCCCTATATATGTA	540
QY	512	TGATCAACAAACCAACGAGCAACACATAGACCTGTCTGCACCTCAACAGTTGGATG	571
Db	541	TTGTATACACAGTTCCATGAGGGGAGCACCACCGCTGCATGACACTTCCACCGTGTATC	600
QY	572	AACCTCAATCTATTTAAGTGTACACACCTAAT	602
Db	601	TATTTGACACACTTGTGGCTTACGACACAGT	631
RESULT 5	877 bp	linear	EST 12-MAR-2001
LOCUS	BG402029		
DEFINITION	60246674871 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4594810 5',		
ACCESSION	BG402029		
VERSION	BG402029.1	GI:13295477	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 877)		
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/ .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: CLONTECH Laboratories, Inc.		
	cDNA Library Preparation: CLONTECH Laboratories, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/ULNL at:		
	http://image.llnl.gov		
	Plate: LUCM1336 row: p column: 11		
	High quality sequence spot: 542.		
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source	1. 877		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:4594810"		
	/clone_lib="NIH_MGC_75"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site:1; SfiI (ggcgccgcgcgc); Site:2: SfiI (ggcgccgcgcgc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCATTAATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCCGAGCGCCGACGATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."		
BASE COUNT	198 a 221 c 199 g 259 t		
ORIGIN			
Query Match	10.8%; Score 109.4; DB 12; Length 877;		
Best Local Similarity	58.5%; Pred. No. 7; 9e-21;		
Matches 210; Conservative 0; Mismatches 146; Indels 3; Gaps 1;			
QY	55	GCTGCTTTTGGAAATTCAGATGATAAATCCACCAAGATGACACTTCTCCCTGT	114
Db	125	GCAACTTGCAAAATACCTGGCTGGCAGCAGAGCTCCCTCGAAAGTACTACTTCCATT	184
QY	115	ATTATGCAATATCTTCTCTGCTGGGATTTCCAGCAGCATGCAATGATGATTCACATTAC	174

[illegible]

Db 335 TCCAGTTCACACGACCCACGCTACATCCTCTTCATACACCGGGTCTTGAGCA 394
 OY 152 ATGACGTAGTGAATATCCACTTATTCATTTTAAATGAGACCTTGAGAGACGACATCA 211
 Db 395 AAGCGTGGCCATCTGATGATGCTTCTTCCACATGCGCGGAGCGGATCTCGGTG 454
 OY 212 TTATGTGACCTGGGCTGACAGATCTCTGTATTCAGACGACCTCCCTTCGTATTC 271
 Db 455 AATGTTCACCTGGCTGCGGAGCTTCTGTATTCCTCCACGCGCCCGCCCTATCT 514
 OY 272 ACTACATGCGACGTGGCGAAACGTGATTTTGAGATTCATGTGTAAAGTTATCCGCT 331
 Db 515 TCTACTACTTCACAAACACGACGTCTGCGGAGCGTCAATGTGCAAGCTGCAGAGGT 574
 OY 332 TCAGCTTCATTTCAACCTGTATAGAGATCTCTCTCCACCTCTTCAGATCTCC 391
 Db 575 TCAATTTCCAGCTGAACCTCTACGGCAGATCTCTNNCCCTACGTCATAGCGGTNNCA 634
 OY 392 GCTACTGTGTGATTCATTCACCCAAATGA 418
 Db 635 GGATACGGGGCGTCTGNNCCCGCTGA 661

RESULT 7
 CENS0532S 1101 bp DNA linear GSS 26-JUL-2000
 LOCUS Tetradon nigroviridis genome survey sequence T7 end of clone
 DEFINITION 020M21 of library A from Tetradon nigroviridis, genomic survey
 sequence.

ACCESSION AL318925
 VERSION AL318925.1 GI:9551809
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetradon nigroviridis.
 ORGANISM Tetradon nigroviridis.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetradon.

REFERENCE 1 (bases 1 to 1101)
 Roest Crolius, H., Jallion, O., Dasilva, C., Bouneau, L., Fisher, C.,
 Bernot, A., Fizames, C., Winkler, P., Brothier, P., Quetier, F.,
 Saurin, W., and Weissenbach, J.
 Estimate of human gene number provided by genome-wide analysis
 using Tetradon nigroviridis DNA sequence
 Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL MEDLINE
 PUBMED 10835645
 REFERENCE 2 (bases 1 to 1101)
 Crolius, H., Jallion, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C.,
 Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W.,
 Bernot, A., and Weissenbach, J.
 Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetradon nigroviridis
 Genome Res. 10 (7), 939-949 (2000)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 TITLE
 JOURNAL
 COMMENT
 This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetradon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetradon.
 Location/Qualifiers

FEATURES
 source
 1. .1101
 /organism="Tetradon nigroviridis"
 /db_xref="taxon:99883"
 /clone="020M21"
 /clone_11b="A"
 /note="Genoscope sequence ID : COAA020AG11C1-end : T7"
 BASE COUNT 305 a 216 c 280 g 284 t 16 others
 ORIGIN

Query Match 10.6%; Score 107.4; DB 17; Length 1101;
 Best Local Similarity 54.0%; Pred. No. 3.4e-20;
 Matches 258; Conservative 0; Mismatches 216; Indels 4; Gaps 2;

OY 92 TCAAGATGACACTACCTCCCTGTATTTATGAGCATATTCCTCTGAGGATTTCCAGGCA 151
 Db 507 TCAAAATACATCCCTGCGCCGCTGCTATGAGCGCTTGTCTTGCTTATCTCA 448
 OY 152 ATGCACTAGTATATCCACTTACATTTTCAAATAGACCTTGGAGAGACGACCATCA 211
 Db 447 ACGCCACAGCCCTGT---GGCTCTTCTGAAATGCGGCGCTGGAACCCACACCCGCT 391
 OY 212 TTATGCTGAACCGGCTGACAGATCTGTGTATTCAGACACCCCTCCCTTCATTC 271
 Db 390 TCTGTGTCCACCTGCGCTCTCCGACTTCTTCAATCTGTGCGTGGCCACCTCATCT 331
 OY 272 ACTACTATGACAGTGGCGAAACACTGATCTTTGGAGATTTCAATGTATGATTCGCT 331
 Db 330 ACTATTACGCCAACACAGGCGCACTGG--CCTTGGCGTGGGAGCTGCAAAATGTGGCT 272
 OY 332 TCAGCTTCATTTCAACCTGTATAGCAGATCTCTTCTCCTACCTGTTTCAGATCTTC 391
 Db 271 TCCCTTCTTACGTCACACTCTACTGAGATCTCTTCTTCCACCTGCATCAGCGGTAC 212
 OY 392 GCTACGTGTGATTCATTCACCCAAATGAGTGTCTTTCATTCACAAACGATGTGCAG 451
 Db 211 GTTACGTGGCATCTCCACCCGATTAAGCGCTGATCTGTGAANCCCGGNAATTCCT 152
 OY 452 TTGTACCTGTGCTGTGTGTGATTCATTTCACTGTAGCTGATTCGATCCGATCCCTTC 511
 Db 151 ACCTGGTGTGGCGCTGCTGTGTGGTGTGATGATGCTGTGGGCTGAACCTCATCT 92
 OY 512 TGTATCATTCACCAACAGACGACCAAGATCAGCTGTCTGCACTTCCAGATTCGGA 569
 Db 91 TTGTACCACTTCCAGCGGAGCAATATCCCTGTGCATGATTCACACNNGCCGGA 34

RESULT 8
 LOCUS BG712193 491 bp mRNA linear EST 08-MAY-2001
 DEFINITION pglin.pk011.f3 Normalized Liver Library Gallus gallus cDNA clone
 pglin.pk011.f3 5' similar to gblAAC60339.1 (AF031897) 6 protein
 coupled P2X nucleotide receptor [Meleagris gallopavo]G, mRNA
 sequence.
 ACCESSION BG712193
 VERSION BG712193.1 GI:14006135
 KEYWORDS EST.
 SOURCE chicken.
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 491)
 Burnside, J., Morgan, R.W., and Cogburn, L.A.
 Chicken ESTs from a normalized liver library
 Unpublished (2001)
 CONTACT: Joan Burnside
 Molecular Endocrinology
 University of Delaware
 40 Townsend Hall, Newark, DE 19717, USA
 Tel: 302 831-1345
 Fax: 302-831-3411
 Email: joan@udel.edu, www.chickest.udel.edu.
 Location/Qualifiers

FEATURES
 source
 1. .491
 /organism="Gallus gallus"
 /db_xref="taxon:9031"
 /clone="pglin.pk011.f3"
 /clone_11b="Normalized Liver Library"
 /sex="Male and Female"
 /tissue_type="liver"
 /lab_host="E.coli EMDH10B"

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/notes: origin: kidney; vector: pME18S-FLS; site_1: DraIII
(CACTGTCTG); site_2: DraIII (CACCATCTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCCTTTTTTTTTTTTTTT]; double-stranded cDNA was

```


DB 488 GATCGTGAACCCCATGGGACACCCAGAGAACCAACATCCGCTGGCTCCTT 547
462 TCGTGTGCTGATGATTCATTCACCTGCTGCTC 495
DB 548 GGCAATCTGGCTCCTGATTTTCTGCTGCATC 581

RESULT 15

A2953874

LOCUS A2953874 606 bp DNA linear GSS 27-APR-2001

DEFINITION 2M0219117F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

ACCESSION A2953874

VERSION A2953874.1 GI:13825101

KEYWORDS

GSS

SOURCE

house mouse.

Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0219 row: L column: 17

Seq primer: CGTGTAAACGACGCGCAT

Class: plasmid ends

High quality sequence stop: 606.

Location/Qualifiers

1. 606

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0219117"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (q114732114[gb|AF129072.1]), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

ORIGIN

100 a 203 c 145 g 158 t

Best Local Similarity 57.2%; Pred. No. 1.1e-17;
Matches 199; Conservative 0; Mismatches 146; Indels 3; Gaps 1;
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DB 277 TATGCGAGTGGGAAACCTGATCTTTGAGATTCATGATGATTTGCGCTTCAC 336
220 TACGCGAGTGGGAAACCTGATCTTTGAGATTCATGATGATTTGCGCTTCAC 279
DB 337 TTCCATTTCAACCTGATATAGACAGATCCCTCTTCACCTGTTGACATTCGCTAC 396
280 TTCTATGCGAATCTATATGACAGATCCCTCTTCACCTGATATGATTCACGCTAC 339
DB 397 TGTGATCATTCACCCATGAGCTGCTTTTCATTCACAAACCTGATGCTACAT 453
340 CTGGCATCTGCGACCCCTGCTTCCTGCGACAAAGCGTGAAGTGGCTGCTGCTGG 399
DB 454 GTAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 513
400 GTAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 459
DB 514 ATCAGATCAACCAACGACGACCAACAGATCAGCTGCTGCTGCTGCTGCTGCTG 561
460 GCTGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 507

Search completed: May 29, 2003, 23:40:16
Job time : 1751 secs

Query Match

9.7%; Score 98.4; DB 17; Length 606;

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55 GCTGCTTTTGGAAATTGCACCTGATGAAACATCCCACTCAAGATGCACCTACCTCCCTGTT 114

; LENGTH: 1842 base pairs

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:
: CLASSIFICATION: 536
:
: PRIOR APPLICATION DATA:

```

APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-41

Query Match 9.9%; Score 100; DB 3; Length 984;
Best local Similarity 57.5%; Pred. No. 6,1e-21;
Matches 200; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

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277 TATGCCAGTGGGAAACATGATCTTGGAGATTTATGTGATTTATCCGCTCAGC 336
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256 TACGCCAGAGGGGACCACTGGCTTGGAGACCTGCGCTTGTAGCGCTTCTC 315
337 TTCCATTTACCTGTATAGACATCTTCTCCTACCTGTTTTCAGATCTTCCGCTAC 396
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316 TTCTATGCCAATCTACATGCGACATCTGTTCTCCTACCTGATTTAGCTTCCAGCGCTAC 375
397 TGTGTGATCATTCACCAATGAGCTGCTTTTCCATTACAAAATCGATGCGAGTT--- 453
376 CTGGGATCTGCCACCCCTGGCTTCTGACAAACGAGAGTGGCGCTGCTGTGG 435
454 GTAGCTGTGAGTGTGATGATTTACATGCTGATGCTGATTTCCGATGACCTTCTG 513
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436 GTAGTGTGAGTGTGATGCTGCTGCTGAGACGCCAATGCTGCGCCAGGAGTCTTT 495
514 ATACATCAACCAACAGACGACCAAGATGAGCTGTCTGACCTCACC 561

Db 496 GCTGCCACAGCATCCAGCGCACCCGACCTGTGTCTGACGACCTGAGC 543
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US-08-513-974B-370
Sequence 370, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400


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: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/390,301
: FILING DATE: 25-JAN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: ADLER, REID G.
: REGISTRATION NUMBER: 30,988
: REFERENCE/DOCKET NUMBER: 2803-0006.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: TELEEX: 90-4030
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1475 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 232..1416
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 232
: US-08-476-000-1

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Query Match          9.68; Score 97.8; DB 1; Length 1475;
Best Local Similarity 52.68; Pred. No. 3.6e-20;
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

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: 91 CTCAGATGACACTACCTCCCTGTTATTTATGACATTATCTCCGCGGATTTCCAGGC 150
: 442 CTGACCAAGGCTCTTTCTCCGGTCGCTACATTATTTGTGTTGATGGTTGGCCAGT 501
: 151 AATGCACTAGTATATCCACTTACATTTCMAAATGAGACCTTGAAGACAGCACCATC 210
: 502 AATGCAATGGCCCTCGATCTTCCTTTCCGAAGAAAGAAACACCCCGCGTAT 561
: 211 ATTATGCTGAACCTGGCTGACAGATCTGCTATCTGACAGCCTCCCTTCCTGATT 270
: 562 TACATGGCAACCTGGCTGGCCGACCTCTCTCTGTCAATCGTGGTCCCCCTGAAGATC 621
: 271 CACTACTATGACGATGCGAAGAACTGGATCTTTGGAGATTTCATGTTAGTTATCCGC 330
: 622 TCCTACCACTAATATGCAACAACTGGGTCTAGGGGAGGCCCTGTGCAAGGTGCTATT 681
: 331 TTCAGCTTCATTCAACCTGTATAGCAGATCTCTTCTCACTGTTTTCAGACATCTTC 390
: 682 GGCCTTTTCTATGTAATGATGTAATGCTCATCTCTTCAATGACCTGCTCAGGTGAC 741
: 391 CGCTACTGTGTATCATTCACCCCAATGAGCTGCTTTTCCATTACAAAATCGATGCGA 450
: 742 AGGTACTGGGTGATCGGAACCCCATGGGACCCCGAAGAAAGCAATCGCGGT 801
: 451 GTTGTAGCCTGCTGTGGTGGATCATTTCACTGTTAGTCTGTC 495
: 802 GCGCTCTCTTGGCAATCTGCTCTGATTTTCTGTGTCACATC 846
: Db

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: RESULT 10
: US-08-472-840-1
: Sequence 1, Application US/08472840
: Patent No. 5763575
: GENERAL INFORMATION:
: APPLICANT: SUNDELIN, JOHAN
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
: TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500

```

```

: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/472,840
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/390,301
: FILING DATE: 25-JAN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: ADLER, REID G.
: REGISTRATION NUMBER: 30,988
: REFERENCE/DOCKET NUMBER: 2803-0006.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: TELEEX: 90-4030
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1475 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 232..1416
: FEATURE:
: NAME/KEY: mat_peptide
: LOCATION: 232
: US-08-472-840-1

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Query Match          9.68; Score 97.8; DB 1; Length 1475;
Best Local Similarity 52.68; Pred. No. 3.6e-20;
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

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: 91 CTCAGATGACACTACCTCCCTGTTATTTATGACATTATCTCCGCGGATTTCCAGGC 150
: 442 CTGACCAAGGCTCTTTCTCCGGTCGCTACATTATTTGTGTTGATGGTTGGCCAGT 501
: 151 AATGCACTAGTATATCCACTTACATTTCMAAATGAGACCTTGAAGACAGCACCATC 210
: 502 AATGCAATGGCCCTCGATCTTCCTTTCCGAAGAAAGAAACACCCCGCGTAT 561
: 211 ATTATGCTGAACCTGGCTGACAGATCTGCTATCTGACAGCCTCCCTTCCTGATT 270
: 562 TACATGGCAACCTGGCTGGCCGACCTCTCTCTGTCAATCGTGGTCCCCCTGAAGATC 621
: 271 CACTACTATGACGATGCGAAGAACTGGATCTTTGGAGATTTCATGTTAGTTATCCGC 330
: 622 TCCTACCACTAATATGCAACAACTGGGTCTAGGGGAGGCCCTGTGCAAGGTGCTATT 681
: 331 TTCAGCTTCATTCAACCTGTATAGCAGATCTCTTCTCACTGTTTTCAGACATCTTC 390
: 682 GGCCTTTTCTATGTAATGATGTAATGCTCATCTCTTCAATGACCTGCTCAGGTGAC 741
: 391 CGCTACTGTGTATCATTCACCCCAATGAGCTGCTTTTCCATTACAAAATCGATGCGA 450
: 742 AGGTACTGGGTGATCGGAACCCCATGGGACCCCGAAGAAAGCAATCGCGGT 801
: 451 GTTGTAGCCTGCTGTGGTGGATCATTTCACTGTTAGTCTGTC 495
: 802 GCGCTCTCTTGGCAATCTGCTCTGATTTTCTGTGTCACATC 846
: Db

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: RESULT 11
: US-08-476-976-1

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[illegible]

211 ATTATGCTGAACCTGGCCGTGACAGATCTGTAATGACCAAGCTCCCTTCCTGAAT 270

Db 562 TACATGGCAACCTGGCCTTGGCCGACCTCTCTGTATCTGTGTTCCCTGGAAGATC 621
QY 271 CACTACTATGCCAGTGGCCGAAAACCTGGATCTTGGAGATTTCATGTGTAAGTTATCCG 330
Db 622 TCCCTACACCTACATGCAACAACCTGGGCTTACGGGAGGCCCTGTGCAAGGTCAT 681
QY 331 TTCAGTTCATTTCAACCTGTATACAGACATCTCTTCCTACCTGTTTACAGATCTTC 390
Db 682 GGCCTTTTCTATGTATACATGTATTTGCTTCATCTCTTTCATGACCTGCTCAGCTGAC 741
QY 391 CGCTACTGTGTATCATTTCAACCAATGAGCTGCTTTTCATTCACAAACTGCATGCA 450
Db 742 AGCTACTGGGTATCGTGAACCCCATGGGACACCCAGGAAGAAGCAACATGCGCGTT 801
QY 451 GTTGAGCTGTCTGCTGTGTGTGATCATTTCTACTGCTGCTGTC 495
Db 802 GGGCTCTCTTGGCAATCTGGCTCTGATTTTCTGTGTCACATC 846

RESULT 13

US-08-486-673B-1
; Sequence 1, Application US/08486673B
; Patent No. 6297026
; GENERAL INFORMATION:
; APPLICANT: Sundellin, Johan
; TITLE OF INVENTION: Nucleic Acids Encoding the C140 Receptor
; FILE REFERENCE: 44481-5006-08-05
; CURRENT APPLICATION NUMBER: US/08/486, 673B
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/097, 938
; PRIOR FILING DATE: 1993-07-26
; PRIOR APPLICATION NUMBER: PCT/US94/08536
; PRIOR FILING DATE: 1994-07-26
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1416)
; OTHER INFORMATION: C140 receptor, genomic DNA and deduced protein
; OTHER INFORMATION: sequences
US-08-486-673B-1

Query Match 9.6%; Score 97.8; DB 4; Length 1475;

Best Local Similarity 52.6%; Pred. No. 3.6e-20;

Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 91 CTCAGATGACACTCTCTGTTATTTATGGCATTAATCTCTCTGGATTTCCAGGC 150
Db 442 CTGACCAAGGCTCTTCTCCGGTCTCTACATTAATGTTGATGGTTGCCAGT 501
QY 151 AATGAGTATGATATTCATTTCAAAATGAGACCTTGGAGAGACAGACATC 210
Db 502 AATGGCATGGCCCTGTGATCTTCTTCCGAAGGAAGAAACACCCCGCGTGAAT 561
QY 211 AATATGCTGAACCTGGGCTGACAGATCTGTATGTGACAGCTCCCTTCCTGATT 270
Db 562 TACATGGCAACCTGGGCTTGGCCGACCTCTCTCTCTCATCTGTGTTCCCTGAAATC 621
QY 271 CACTACTATGCCAGTGGCGAAAACCTGGATCTTTGGAGATTTCATGTGTAAGTTATCCG 330
Db 622 TCCATACACCTACATGCAACAACCTGGGCTTACGGGAGGCCCTGTGCAAGTGTGAT 681
QY 331 TTAGCTTCATTTCAACCTGTATAGAGATCTCTCTCTCACTGTTTCAAGATCTTC 390
Db 682 GGGCTTTTCTATGTATACATGTATTTGCTTCATCTCTTTCATGAGACCTGCTCAGGTCAG 741
QY 391 CGTACTGTGTATCATTTCAACCAATGAGCTGTTTTCATTCACAAACTGCATGTGA 450

Db 742 AGCTACTGGGTATCGTGAACCCCATGGGACACCCAGGAAGAAGCAACATGCGCGTT 801
QY 451 GTTGAGCTGTCTGCTGTGTGTGATCATTTCTACTGCTGCTGTC 495
Db 802 GGGCTCTCTTGGCAATCTGGCTCTGATTTTCTGTGTCACATC 846

RESULT 14

US-08-476-000-60
; Sequence 60, Application US/08476000
; Patent No. 5716789
; GENERAL INFORMATION:
; APPLICANT: SUNDELLIN, JOHAN
; TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
; NUMBER OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476, 000
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/390, 301
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ADLER, REID G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 2803-0006.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2732 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..1269
US-08-476-000-60

Query Match 9.6%; Score 97.8; DB 1; Length 2732;

Best Local Similarity 52.6%; Pred. No. 5.1e-20;

Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 91 CTCAGATGACACTCTCTGTTATTTATGGCATTAATCTCTCTGGATTTCCAGGC 150
Db 295 CTGACCAAGGCTCTTCTCCGGTCTCTACATTAATGTTGATGGTTGCCAGT 354
QY 151 AATGAGTATGATATTCATTTCAAAATGAGACCTTGGAGAGACAGACATC 210
Db 355 AATGCATGGCCCTGTGATCTTCTTCCGAAGGAAGAAACACCCCGCGTGAAT 414
QY 211 AATATGCTGAACCTGGGCTGACAGATCTGTATGTGACAGCTCCCTTCCTGATT 270
Db 415 TACATGGCAACCTGGGCTTGGCCGACCTCTCTCTCTCATCTGTGTTCCCTGAAATC 474
QY 271 CACTACTATGCCAGTGGCGAAAACCTGGATCTTTGGAGATTTCATGTGTAAGTTATCCG 330

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Db      475 TCCTACCACTTACATGGCAACACTGGGTCTACGGGGGGGCGCTGTGCAAGGTGCTCATTT 534
Qy      331 TTCAGCTTCCATTTCAACCTGTATAGCAGCATCCCTCCCTCAGCTGTATAGCATCTTC 390
Db      535 GGCCTTTTCTATGTGTAACATGTATATGCTCCATCTCTTCATGACCTGCTTACGGGTGAG 594
Qy      391 CGCTACTGTGTGATCATTCACCAATGAGCTGCTTTCCATTCACAAAACCTGATGTGCA 450
Db      595 AGGTACTGGGTGATCGTAACCCATGGGACACCCAGAGAAAGGCAAAACATGCGCGTT 654
Qy      451 GTTGTAGCCTGTGCTGTGTGTGTGATCATTTTCACTGGTGTGTC 495
Db      655 GCGCTCTCTTGGAATCTGGCTCTGATTTTCTGGTCAACATC 699

RESULT 15
US-08-472-840-60
; Sequence 60, Application US/08472840
; Patent No. 5763575
; GENERAL INFORMATION:
; APPLICANT: SUNDELIN, JOHAN
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
; TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,840
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,301
; FILING DATE: 25-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ADLER, REID G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 2803-0006.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2732 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..1269
; US-08-472-840-60

Query Match      9.6%; Score 97.8; DB 1; Length 2732;
Best Local Similarity 52.6%; Pred. No. 5.1e-20;
Matches 213; Conservative 0; Mismatches 192; Indels 0; Gaps 0;
Qy      91 CTCAGATGCACTACTCCCTGTTATTTATGGCAATTCCTCTCGTGGGATTTCCAGGC 150
Db      295 CTGACCAACGGCTTCTTCGCGTGTCTACATTTATGTGTGTGATGTGTTGCCAGT 354
Qy      151 AATGCACTAGTATATCACTTACATTTTCAAAAATGAGACCTTGAAGAGCAGCACCATC 210

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Db      355 AATGGCATGGCCCTCTGTGATCTCTTTTCGAACGAGAAAGAAACACCCGCGTGATT 414
Qy      211 AATTAGCTGAACCTGGCCCTGCAGCAAGATCTGTATCTGACACGCTCCCTTCGTGATT 270
Db      415 TACATGGCCAACTGGCTTGTGGCGACCTCTCTCTGTGATCTGTGTTCCCTCAAGATC 474
Qy      271 CACTACTATGCACTGGCGAAACGTGATCTTTGGAGATTTTCATGTGTAACTTATCCGC 330
Db      475 TCCTACCACTTACATGGCAACACTGGGTCTACGGGGGGGCGCTGTGCAAGGTGCTCATTT 534
Qy      331 TTCAGCTTCCATTTCAACCTGTATAGCAGCATCCCTCTTCATGACCTGTTTATAGCATCTTC 390
Db      535 GGCCTTTTCTATGTGTAACATGTATATGCTCCATCTCTTCATGACCTGCTCAGGTCGAG 594
Qy      391 CGCTACTGTGTGATCATTCACCAATGAGCTGCTTTCCATTCACAAAACCTGATGTGCA 450
Db      595 AGGTACTGGGTGATCGTAACCCATGGGACACCCAGAGAAAGGCAAAACATGCGCGTT 654
Qy      451 GTTGTAGCCTGTGCTGTGTGTGTGATCATTTTCACTGGTGTGTC 495
Db      655 GCGCTCTCTTGGAATCTGGCTCTGATTTTCTGGTCAACATC 699

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Search completed: May 29, 2003, 23:41:32
 Job time : 66 secs

Alignment Scores:

Refd. No.: 1.5e-158 Length: 1014
 Seqre: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-023-775b-2 (1-337) x US-10-023-775b-1 (1-1014)

QY 1 MetLsnGluPLeuAspTYrLeuAlaAsnAlaSerAspPheProAspTYrAlaAlaAla 20
 DB 1 ATGATAGCCAGCAGCATTATAGCAAAATCCTTGATTTCCCGGATATAGCAGCTGCT 60
 QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisTYrLeuProValIleTYr 40
 DB 61 TTGGAGATTCAGTGTAGAAACATCCCACTCAAGATGACACTGCTGCTGATTTAT 120
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTYrIlePhe 60
 DB 121 GGCAATTAATCTCCGCGGGAGATTCCAGGCAATGAGATGATATCCACTTATATTC 180
 QY 61 LysMetArgProTrpLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 181 AAAATGAGACCTTGAGAGACGACACCATATATGCTGAACCTGGCTGCACAGATCTG 240
 QY 81 LeuTYrLeuThrSerLeuProPheLeuIleHisTYrTYrAlaSerGlyAsnTrpIle 100
 DB 241 CTGATCTGACAGCCTTCCTCTCGATTCATCACTATGCGAGGGGAAACCTGGATC 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTYrSerSer 120
 DB 301 TTGGAGATTCAGTGTAGAAATATATCCGCTTACAGCTTCATTCACCTGATATAGCAGC 360
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTYrCysValIleIleHisPrometSer 140
 DB 361 ATCCCTCTCCCTCACCCTGTTTCAGCATTTCCGCTACTGTCATTCATCCACCATGAGC 420
 QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValIleTrpIleIle 160
 DB 421 TGCCTTTCATTCACAAACGATGTCATATGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCATAGTACGCTGATCCGATGACCTCTTGATGACATCAACCAACAGACCAACAGCA 540
 QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTYrAsnLeu 200
 DB 541 TCAGCTGTCTCGACCTCACCAGTTCGATGACATCAATATGATATGATGATGATGATGAT 600
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTYrThrThr 220
 DB 601 ATTTGACTGCAACACTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuLysGlyLysAlaArg 240
 DB 661 ATTTATCCACTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 720
 QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTYrValCysPheLeuProPheHisIleLeu 260
 DB 721 AGGGAACCAATTCGCTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 261 ArgValIleArgGlyLeuSerArgLeuLeuSerIleSerCysSerIleGluAsnAlaIle 280
 DB 781 AGGTCATTCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 840
 QY 281 HisGluAlaTYrIleValSerArgProLeuAlaIleLeuAsnThrPheGlyAsnLeuVal 300
 DB 841 CATGAGCTTACATGCTGTCTGACCATTAAGCTGCTGCAACACCTTGGTACCTGCTTA 900
 QY 301 LeuTYrValValIleSerAspAsnPheGlnAlaValCysSerThrValArgCysLys 320
 DB 901 CTATATGT 960

QY 321 ValSerGlyAsnLeuGlnAlaIleLysIleSerTYrSerAsnAspPro 337
 DB 961 GTAAAGCGGAGACCTTGAGCAAGCAAGCAAAATTAATGATTACTCAACCAACCT 1011

RESULT 2

US-10-144-1
 : Sequence 1, Application US/10270144
 : Publication No. US20030049790A1

GENERAL INFORMATION:

: APPLICANT: MET, Ming-Hui et al
 : TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
 : TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
 : FILE REFERENCE: C100075000N
 : CURRENT APPLICATION NUMBER: US/10/270,144
 : PRIOR FILING DATE: 2002-10-15
 : PRIOR FILING DATE: 2000-05-18
 : NUMBER OF SEQ ID NOS: 7
 : SOFTWARE: FASTSEQ for Windows Version 4.0
 : SEQ ID NO 1
 : LENGTH: 1014
 : TYPE: DNA
 : ORGANISM: Human
 : US-10-270-144-1

Alignment Scores:

Pred. No.: 1.5e-158 Length: 1014
 Score: 1771.00 Matches: 337
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-023-775b-2 (1-337) x US-10-270-144-1 (1-1014)

QY 1 MetLsnGluPLeuAspTYrLeuAlaAsnAlaSerAspPheProAspTYrAlaAlaAla 20
 DB 1 ATGATAGCCAGCAGCATTATAGCAAAATCCTTGATTTCCCGGATATAGCAGCTGCT 60
 QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisTYrLeuProValIleTYr 40
 DB 61 TTGGAGATTCAGTGTAGAAACATCCCACTCAAGATGACATRCCTCCGATATAT 120
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTYrIlePhe 60
 DB 121 GGCAATTAATCTCCGCGGGAGATTCCAGGCAATGAGATGATATCCACTTATATTC 180
 QY 61 LysMetArgProTrpLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 DB 181 AAAATGAGACCTTGAGAGACGACACCATATATGCTGAACCTGGCTGCACAGATCTG 240
 QY 81 LeuTYrLeuThrSerLeuProPheLeuIleHisTYrTYrAlaSerGlyAsnTrpIle 100
 DB 241 CTGATCTGACAGCCTTCCTCTCGATTCATCACTATGCGAGGGGAAACCTGGATC 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTYrSerSer 120
 DB 301 TTGGAGATTCAGTGTAGAAATATATCCGCTTACAGCTTCATTCACCTGATATAGCAGC 360
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTYrCysValIleIleHisPrometSer 140
 DB 361 ATCCCTCTCCCTCACCCTGTTTCAGCATTTCCGCTACTGTCATTCATCCACCATGAGC 420
 QY 141 CysPheSerIleHisLysThrArgCysAlaValAlaCysAlaValIleTrpIleIle 160
 DB 421 TGCCTTTCATTCACAAACATCCGATGACCTCTTGATGACATCAACCAACAGACCAACAGCA 480
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 DB 481 TCATAGTACGCTGATCCGATGACCTCTTGATGACATCAACCAACAGACCAACAGCA 540

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QY 181 SerAlaCysLeuAspLeuThrSerSerAspGluLeuAsnThrIleLysTrpTyrAsnLeu 200
 |||||
 DB 541 TCAGCTGCTGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 600
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 |||||
 DB 601 ATTATGACGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuGlnLysAlaArg 240
 |||||
 DB 661 ATTATGACGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 720
 QY 241 ArgLeuThrIleLeuLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 |||||
 DB 721 AGGCTACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 |||||
 DB 781 AGGCTACCTGCGATGCAATCTGCGCTGCTGCAATGCTGCTGCTGCAATGCAATGCAATG 840
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaIleAsnThrPheGlyAsnLeuLeu 300
 |||||
 DB 841 CANGAAGCTTACATCTGCTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 QY 301 LeuTyrValValValSerAspAsnPhenGlnAlaValCysSerThrValArgCysLys 320
 |||||
 DB 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 321 ValSerGlyAsnLeuGlnAlaLysIleSerTyrSerAsnAsnPro 337
 |||||
 DB 961 GTAAGGGGAGACCTTGAGCAAGCAAGAAATAGTTACTCAACAACCT 1011

RESULT 3

US-10-188-405-7

Sequence 7, Application US/10188405

Publication No. US20030082585A1

GENERAL INFORMATION:

APPLICANT: Tian, Hui

APPLICANT: Dai, Kang

APPLICANT: Chen, Jin-Long

APPLICANT: Zhao, Jiaqiang

APPLICANT: Cutler, Gene

APPLICANT: Tularik, Inc.

TITLE OF INVENTION: No. US20030082585A1el Receptors

FILE REFERENCE: 018781-00841005

CURRENT APPLICATION NUMBER: US/10/188,405

PRIOR FILING DATE: 2002-07-01

PRIOR APPLICATION NUMBER: US 60/302,800

NUMBER OF SEQ. ID NOS: 25

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 1014

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: OTHER INFORMATION: human TGR164

US-10-188-405-7

Alignment Scores:

Pred. No.: 1,56-158

Score: 1771,00

Percent Similarity: 100,00%

Best Local Similarity: 100,00%

Query Match: 100,00%

DB: 9

US-10-023-775B-2 (1-337) x US-10-188-405-7 (1-1014)

QY 1 MetAsnGluProLeuAspTyrLeuValAsnAlaSerAspPheProAspTyrAlaAla 20
 |||||
 DB 1 ATGATGAGCCACTAGACTATTTAGCAAAATGCTTCTGATTTTCCCATTTATGACGCTGCT 60

QY 21 PheGlyAsnCysThrAspGluAsnIleProLeuLysMetHisTyrLeuProValIleTyr 40
 |||||
 DB 61 TTGGAAATGCACTGATGAAACATCCATCAATGACATGCTGCTGCTGCTGCTGCTGCTGCTG 120
 QY 41 GlyIleIlePheLeuValGlyPheProGlyAsnAlaValIleSerThrTyrIlePhe 60
 |||||
 DB 121 GGCATTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 QY 61 LysMetArgProTyrLysSerSerThrIleIleMetLeuAsnLeuAlaCysThrAspLeu 80
 |||||
 DB 181 AAATGAGACCTGGAAGAGACACCATCATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
 QY 81 LeuTyrLeuThrSerLeuProPheLeuIleHisTyrTyrAlaSerGlyLysAsnTrpIle 100
 |||||
 DB 241 CTGATCTACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 QY 101 PheGlyAspPheMetCysLysPheIleArgPheSerPheHisPheAsnLeuTyrSerSer 120
 |||||
 DB 301 TTTCAGATTTCTGATGTAAGTTTATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 QY 121 IleLeuPheLeuThrCysPheSerIlePheArgTyrCysValIleIleHisProMetSer 140
 |||||
 DB 361 ATCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 141 CysPheSerIleHisTyrArgCysAlaValAlaCysAlaValAlaTrpIleIle 160
 |||||
 DB 421 TCTTTTCCATTCACAAACCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 161 SerLeuValAlaValIleProMetThrPheLeuIleThrSerThrAsnArgThrAsnArg 180
 |||||
 DB 481 TCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
 QY 541 TCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
 DB 601 ATTTGACGCAACTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 201 IleLeuThrAlaThrThrPheCysLeuProLeuValIleValThrLeuCysTyrThrThr 220
 |||||
 DB 601 ATTTGACGCAACTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 QY 221 IleIleHisThrLeuThrHisGlyLeuGlnThrAspSerCysLeuGlnLysAlaArg 240
 |||||
 DB 661 ATTATGACGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG 720
 QY 241 ArgLeuThrIleLeuLeuLeuAlaPheTyrValCysPheLeuProPheHisIleLeu 260
 |||||
 DB 721 AGGCTACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 QY 261 ArgValIleArgIleGluSerArgLeuLeuSerIleSerCysSerIleGluAsnGlnIle 280
 |||||
 DB 781 AGGCTACCTGCGATGCAATCTGCGCTGCTGCAATGCTGCTGCTGCAATGCAATGCAATG 840
 QY 281 HisGluAlaTyrIleValSerArgProLeuAlaIleAsnThrPheGlyAsnLeuLeu 300
 |||||
 DB 841 CANGAAGCTTACATCTGCTTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 QY 301 LeuTyrValValValSerAspAsnPhenGlnAlaValCysSerThrValArgCysLys 320
 |||||
 DB 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 QY 321 ValSerGlyAsnLeuGlnAlaLysIleSerTyrSerAsnAsnPro 337
 |||||
 DB 961 GTAAGGGGAGACCTTGAGCAAGCAAGAAATAGTTACTCAACAACCT 1011

RESULT 4

US-09-885-453-2

Sequence 2, Application US/09885453

Publication No. US2003008080A1

GENERAL INFORMATION:

APPLICANT: Communi, Didier

TITLE OF INVENTION: RECEPTOR GPCR10

FILE REFERENCE: 9409/2082

CURRENT APPLICATION NUMBER: US/09/885,453

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Db 121 GGCAATATCTCTCTGTTGGATTTCCAGGCAATGCAATGATGATTCACCTTACATTTTC 180
Qy 181 AAAATGAGACCTTGGAGAGACGACCATCATTAATGCAACCGGCTGACGATCTG 240
Db 181 AAAATGAGACCTTGGAGAGACGACCATCATTAATGCAACCGGCTGACGATCTG 240
Qy 241 CTGTATCTGACGACCTCCCTCTGATTCATGATGCAATGCAATGCAATGCAATG 300
Db 241 CTGTATCTGACGACCTCCCTCTGATTCATGATGCAATGCAATGCAATGCAATG 300
Qy 301 TTGGAGATTTGCAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 360
Db 301 TTGGAGATTTGCAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 360
Qy 361 ATCCCTCTCTGACCTTTTACGATCTTCCGCTGATGATGATGATGATGATGATGAT 420
Db 361 ATCCCTCTCTGACCTTTTACGATCTTCCGCTGATGATGATGATGATGATGATGAT 420
Qy 421 TGGCTTTCCATTCACAAACTGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 480
Db 421 TGGCTTTCCATTCACAAACTGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 480
Qy 481 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Qy 541 TCAGCCGTCTGACGACCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 600
Db 541 TCAGCCGTCTGACGACCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 600
Qy 601 ATTTGACTGCAACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 601 ATTTGACTGCAACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Qy 661 ATTTGACTGCAACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 ATTTGACTGCAACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Qy 721 AGGCTAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 AGGCTAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy 781 AGGCTAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 781 AGGCTAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Qy 841 CATGAAGCTTACATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 841 CATGAAGCTTACATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 900
Qy 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Qy 961 GTAAAGCGGAACTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1014
Db 961 GTAAAGCGGAACTTGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1014

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RESULT 2
US-10-270-144-1
; Sequence 1, Application US/10270144
; Publication No. US20030049790A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C10007500CN
; CURRENT APPLICATION NUMBER: US/10/270,144
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; PRIOR FILING DATE: 2000-05-18

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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1014
; TYPE: DNA
; ORGANISM: Human
US-10-270-144-1
Query Match 99.8%; Score 1012.4; DB 9; Length 1014;
Best Local Similarity 99.9%; Pred. No. 8e-301;
Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
please note that it's 100% actually!
Qy 1 ATGAATGAGCCTAGACCTATTTAGCAAAATGCTTCTGATTTCCCGATTAATGAGCGCT 60
Db 1 ATGAATGAGCCTAGACCTATTTAGCAAAATGCTTCTGATTTCCCGATTAATGAGCGCT 60
Qy 61 TTGGAAATTTGCACTGATGAAATTCACCTCACTCAAGATGCACTACCTCCCTGATTTAT 120
Db 61 TTGGAAATTTGCACTGATGAAATTCACCTCACTCAAGATGCACTACCTCCCTGATTTAT 120
Qy 121 GGCAATATCTCTCTGTTGGATTTCCAGGCAATGCAATGCAATGCAATGCAATGCAAT 180
Db 121 GGCAATATCTCTCTGTTGGATTTCCAGGCAATGCAATGCAATGCAATGCAATGCAAT 180
Qy 181 AAAATGAGACCTTGGAGAGACGACCATCATTAATGCAACCGGCTGACGATCTG 240
Db 181 AAAATGAGACCTTGGAGAGACGACCATCATTAATGCAACCGGCTGACGATCTG 240
Qy 241 CTGTATCTGACGACCTCCCTCTGATTCATGATGCAATGCAATGCAATGCAATGCAAT 300
Db 241 CTGTATCTGACGACCTCCCTCTGATTCATGATGCAATGCAATGCAATGCAATGCAAT 300
Qy 301 TTGGAGATTTGCAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 360
Db 301 TTGGAGATTTGCAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 360
Qy 361 ATCCCTCTCTGACCTTTTACGATCTTCCGCTGATGATGATGATGATGATGATGAT 420
Db 361 ATCCCTCTCTGACCTTTTACGATCTTCCGCTGATGATGATGATGATGATGATGAT 420
Qy 421 TGGCTTTCCATTCACAAACTGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 480
Db 421 TGGCTTTCCATTCACAAACTGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 480
Qy 481 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Qy 541 TCAGCCGTCTGACGACCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 600
Db 541 TCAGCCGTCTGACGACCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 600
Qy 601 ATTTGACTGCAACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 601 ATTTGACTGCAACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Qy 661 ATTTGACTGCAACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 ATTTGACTGCAACTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Qy 721 AGGCTAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 AGGCTAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Qy 781 AGGCTAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 781 AGGCTAACCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Qy 841 CATGAAGCTTACATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 841 CATGAAGCTTACATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 900
Qy 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 CTATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960

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Db 901 CTATATGTGTGTGTACGCGACAACCTTTCAGCAGCGCTGTCTGCTCAACAGTGAATGCGAA 960
 QY 961 GTAAGCGGGAACCTTGAGCGACCAAGAAATTTAGTTACTCAACAACACCTTGA 1014
 Db 961 GTAAGCGGGAACCTTGAGCGACCAAGAAATTTAGTTACTCAACAACACCTTGA 1014

RESULT 3

US-10-188-405-7
; sequence 7, Application US/10188405
; Publication No. US20030082585A1
; PUBLICATION INFORMATION

GENETIC INFORMATION:
 APPLICANT: Tian, Hui
 APPLICANT: Dai, Kang
 APPLICANT: Chen, Jin-Long
 APPLICANT: Zhao, Jiayang
 APPLICANT: Cutler, Gene
 APPLICANT: Twilark Inc.
 TITLE OF INVENTION: NO. US20030082585A1el Receptors
 FILE REFERENCE: 018761-0084100S
 CURRENT APPLICATION NUMBER: US/10/188,405
 CURRENT FILING DATE: 2002-07-01
 PRIOR APPLICATION NUMBER: US 60/302,800
 PRIOR FILING DATE: 2001-07-03
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: Patent Ver. 2.1
 SEQ ID NO 7
 LENGTH: 1014
 TYPE: DNA
 ORGANISM: Homo sapiens
 OTHER INFORMATION: human TGR164
 US-10-188-405-7

Query Match	99.8%	Score 1012.4	DB 9	Length 1014
Best Local Similarity	99.8%	Pred. No. 86-301		
Matches 1013; Conservative	0	Mismatches	1	Indels 0
				Gaps 0

Oy	1	ATGATGAGCAGCTAGACATTTATAGCAAAATGCTTGATTTTCCCGATATGACAGTGT	60
Db	1	ATGAAATGAGCCACATGACTATTTAGCAAAATGCTTGATTTTCCCGATATGACAGTGT	60
Oy	61	TTTGAAATTTGCATGATGAAACATATCCACTCAAGATGACACTACCTCCCTGTTATAT	120
Db	61	TTTGAAATTTGCATGATGAAACATATCCACTCAAGATGACACTACCTCCCTGTTATAT	120
Oy	121	GGCATTAATCTTCCTGGGAGATTTCCAGACAAATGGAGATGATATATCCACTACATTTTC	180
Db	121	GGCATTAATCTTCCTGGGAGATTTCCAGACAAATGGAGATGATATATCCACTACATTTTC	180
Oy	181	AAAAATGAGACCTTGGAGAGCAGCAGCATCATATATGCTGAACCTGGCTGCACAGATCTG	240
Db	181	AAAAATGAGACCTTGGAGAGCAGCAGCATCATATATGCTGAACCTGGCTGCACAGATCTG	240
Oy	241	CTGATCTGACACAGCTCCCTCCCTGATCTCTATATGCGAGTGGCGAAAATCGGATC	300
Db	241	CTGATCTGACACAGCTCCCTCCCTGATCTCTATATGCGAGTGGCGAAAATCGGATC	300
Oy	301	TTTGAGATTTTCATGCTGTAAGTTTATCCGCTTCAGCTTCCATTTTCAACCTGTAATGACAC	360
Db	301	TTTGAGATTTTCATGCTGTAAGTTTATCCGCTTCAGCTTCCATTTTCAACCTGTAATGACAC	360
Oy	361	ATCCCTTTCCTACCTGTTTCAGCATTTCCGCTACGTGATCATTTTACCCCAATGAC	420
Db	361	ATCCCTTTCCTACCTGTTTCAGCATTTCCGCTACGTGATCATTTTACCCCAATGAC	420
Oy	421	TGCTTTTCATTCACAAAACCTGAGTGGCATTTGAAGCTGCTGCTGGTGTGATCATTT	480
Db	421	TGCTTTTCATTCACAAAACCTGAGTGGCATTTGAAGCTGCTGCTGGTGTGATCATTT	480
Oy	481	TCACCTGTAAGCTGTCAATTCGATGACCTTTCTTGATCATCAACCAACGAGCAACAGAC	540
Db	481	TCACCTGTAAGCTGTCAATTCGATGACCTTTCTTGATCATCAACCAACGAGCAACAGAC	540

Db	481	TCACAGTGGTGGTGCATTCGATGCACCTCTTGGATGCATCAACCAACAGACCAACAG	540
QY	541	TCAGCTGCTCTGGACCTACACAGTTCCGGATGAACTCAATATATATAGTGGTCAACCTA	600
Db	541	TCAGCTGCTCTGGACCTACACAGTTCCGGATGAACTCAATATATATAGTGGTCAACCTG	600
QY	601	ATTATGACACAACTACTTTCGTGCTCCCTCTGGTGTAGTGAACACTTTCCTATACACG	660
Db	601	ATTATGACACAACTACTTTCGTGCTCCCTCTGGTGTAGTGAACACTTTCCTATACACG	660
QY	661	ATTATCCACACTCTGACCCATGAGTGCACAACTGACACGCTGCTTAAGCAAGAAAGCAG	720
Db	661	ATTATCCACACTCTGACCCATGAGTGCACAACTGACACGCTGCTTAAGCAAGAAAGCAG	720
QY	721	AGGCTAACCATCTGCTACTGCTTCATCTTAAGTAGTATTTTAAACCTTCATATCTTG	780
Db	721	AGGCTAACCATCTGCTACTGCTTCATCTTAAGTAGTATTTTAAACCTTCATATCTTG	780
QY	781	AGGCTCATTCGGATCGAATCTCGCCTGCTTCAATCAGTGTGTCATGGAATCAAGATC	840
Db	781	AGGCTCATTCGGATCGAATCTCGCCTGCTTCAATCAGTGTGTCATGGAATCAAGATC	840
QY	841	CATTAAGCTTAATGCTTTCTTAGACCACTTACTGCTGCTGAAACACCTTGGTAACCTGA	900
Db	841	CATTAAGCTTAATGCTTTCTTAGACCACTTACTGCTGCTGAAACACCTTGGTAACCTGA	900
QY	901	CTATATGAGTGGTGCAGGACAACTTCTAGCAGGCTGTCTGCTCAACAGTGAAGTGC	960
Db	901	CTATATGAGTGGTGCAGGACAACTTCTAGCAGGCTGTCTGCTCAACAGTGAAGTGC	960
QY	961	GTAAGCGGAACTTGAGAGCAAGCAAAAGAAATTTAGTATCTGTAACCAACCTTGA	1014
Db	961	GTAAGCGGAACTTGAGAGCAAGCAAAAGAAATTTAGTATCTGTAACCAACCTTGA	1014

RESULT 4

US-09-885-453-2
; Sequence 2, Application US/09885453
; Publication No. US20030088080A1

```

1 GENERAL INFORMATION: Didiar
2 APPLICANT: Communi,
3 TITLE OF INVENTION: RECEPTOR GPCR4.10
4 FILE REFERENCE: 9409/2082
5 CURRENT APPLICATION NUMBER: US/09/885,455
6 PRIORITY FILING DATE: 2001-06-20
7 CURRENT APPLICATION NUMBER: US/09/885,453
8 PRIOR FILING DATE: 2001-06-21
9 NUMBER OF SEQ. ID NOS: 12
10 SOFTWARE: PatentIn version 3.1

```

```

? SEQ ID NO: 2
? LENGTH: 1014
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE: ...
? NAME/KEY: DNA nucleotide sequence
? LOCATION: (1)..(1014)
? OTHER INFORMATION: GPCR10 DNA sequence
US-09-885-453-2

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Query Match	99.8%	Score 1012.4;	DB 9;	Length 1014;
Best Local Similarity	99.9%	Pred. No. 8e-301;		
Matches 1013; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

OY 1 ATGATGAGCCACTAGACTATTATTAGCAAAATGCTCTGTGATTTCCCGATTATGACAGCTGT 60
Db 1 ATGATGAGCCACTAGACTATTATTAGCAAAATGCTCTGTGATTTCCCGATTATGACAGCTGT 60			
OY 61 TTGGAATTCACATGATGATGAACAATCCCATCAGATGACACTACCTCCCTATATATAT 120			
Db 61 TTGGAATTCACATGATGATGAACAATCCCATCAGATGACACTACCTCCCTATATATAT 120			
OY 121 GGCATATATCTCTGCTGGGATTTTCACGACCAATGCAAGTAGATGATTCACACTTACATTTTC 180			

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Db 121 ILFLFCSTFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNR 180
Qy 181 SACLDTSSDELNTIKWNLILATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Db 181 SACLDTSSDELNTIKWNLILATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Qy 241 RLTIILLAAVYCFELPHILRVIRIESRLISCSISIQHHEAVIYSRPLAALNTFGNLL 300
Db 241 RLTIILLAAVYCFELPHILRVIRIESRLISCSISIQHHEAVIYSRPLAALNTFGNLL 300
Qy 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337
Db 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337

RESULT 2

US-10-270-144-2
; Sequence 2, Application US/10270144
; Publication No. US20030049790A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NOCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: C1000750CON
; CURRENT APPLICATION NUMBER: US/10/270,144
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: PRF
; ORGANISM: Human
US-10-270-144-2

Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3 2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEPLDYLANASDPDYAAAFGNCNTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60
Db 1 MNEPLDYLANASDPDYAAAFGNCNTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60
Qy 61 KMRPKSSITIMINACTDILYLTSLPFLIHYASGEMNIFGDMCKFIRFSHFNLSS 120
Db 61 KMRPKSSITIMINACTDILYLTSLPFLIHYASGEMNIFGDMCKFIRFSHFNLSS 120
Qy 121 ILFLFCSTFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNR 180
Db 121 ILFLFCSTFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNR 180
Qy 181 SACLDTSSDELNTIKWNLILATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Db 181 SACLDTSSDELNTIKWNLILATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Qy 241 RLTIILLAAVYCFELPHILRVIRIESRLISCSISIQHHEAVIYSRPLAALNTFGNLL 300
Db 241 RLTIILLAAVYCFELPHILRVIRIESRLISCSISIQHHEAVIYSRPLAALNTFGNLL 300
Qy 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337
Db 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337

RESULT 3
US-10-188-405-8
; Sequence 8, Application US/10188405
; Publication No. US20030082585A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Dai, Kang

APPLICANT: Chen, Jin-Long
APPLICANT: Zhao, Jiagang
APPLICANT: Cutler, Gene
APPLICANT: Tularix Inc.
; TITLE OF INVENTION: NO. US20030082585A1a1 Receptors
; FILE REFERENCE: 018/81-00841005
; CURRENT APPLICATION NUMBER: US/10/188,405
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/302,800
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 387
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR164
US-10-188-405-8

Query Match 100.0%; Score 1771; DB 9; Length 337;
Best Local Similarity 100.0%; Pred. No. 3 2e-152;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNEPLDYLANASDPDYAAAFGNCNTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60
Db 1 MNEPLDYLANASDPDYAAAFGNCNTDENIPKMHYLPVYIGIIFLVGPGNAVISTYIF 60
Qy 61 KMRPKSSITIMINACTDILYLTSLPFLIHYASGEMNIFGDMCKFIRFSHFNLSS 120
Db 61 KMRPKSSITIMINACTDILYLTSLPFLIHYASGEMNIFGDMCKFIRFSHFNLSS 120
Qy 121 ILFLFCSTFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNR 180
Db 121 ILFLFCSTFRYCVIIHPMSCFSIHKTRCAVAVCAVWIIISLVAIIPMTFLITSTNR 180
Qy 181 SACLDTSSDELNTIKWNLILATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Db 181 SACLDTSSDELNTIKWNLILATPFCPLVITVLCYTTIIHTLHGLQDSCLOKAR 240
Qy 241 RLTIILLAAVYCFELPHILRVIRIESRLISCSISIQHHEAVIYSRPLAALNTFGNLL 300
Db 241 RLTIILLAAVYCFELPHILRVIRIESRLISCSISIQHHEAVIYSRPLAALNTFGNLL 300
Qy 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337
Db 301 LYVVSNDNFQOAVCSIVRCVSGNLEQAKKISYSNNP 337

RESULT 4

US-09-885-453-1
; Sequence 1, Application US/09885453
; Publication No. US20030088080A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: RECEPTOR GPCRx10
; FILE REFERENCE: 9409/2082
; CURRENT APPLICATION NUMBER: US/09/885,453
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 337
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: amino acid sequence GPCRx10
; LOCATION: (1)-(337)
; OTHER INFORMATION: GPCRx10 amino acid sequence
US-09-885-453-1

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RS Claim 2; Page 30; 37pp; English.

XX The invention relates to an isolated AXOR89 polypeptide (G-protein coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide and polynucleotide encoding the polypeptide, is useful for identifying agonists and antagonists (or inhibitors) that are potentially useful in treating conditions associated with an AXOR89 imbalance, such as bacterial, fungal or protozoan infections, cancers, pain, asthma, Parkinson's disease, diabetes, obesity, anorexia, bulimia, acute heart failure, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hyperplasia, migraine, vomiting, psychotic and neurological disorders, anxiety, schizophrenia, manic depression, delirium, dementia, dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome. The polynucleotide sequence may also be used for chromosome localization or tissue expression studies. The AXOR89 is used as a vaccine or to produce fusion proteins. The present sequence is human AXOR89 cDNA.

XX Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

Query Match 100.0%; Score 1014; DB 24; Length 1014;
Best Local Similarity 100.0%; Pred. No. 7, 1e-289;
Matches 1014; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGAGCCACTACACTATTTAGCAATGCTTTCGATTTCCCGATTATGACGCTGCT 60
DB 1 ATGATGAGCCACTACACTATTTAGCAATGCTTTCGATTTCCCGATTATGACGCTGCT 60
QY 61 TTGGAAATTCGACATGATGAAATGCACTGACATGACATGACATGACATGACATGACAT 120
DB 61 TTGGAAATTCGACATGATGAAATGCACTGACATGACATGACATGACATGACATGACAT 120
QY 121 GGCATATCTCTCCCTGGGATTTCCAGGATGACATGATGATGATGATGATGATGATGAT 180
DB 121 GGCATATCTCTCCCTGGGATTTCCAGGATGACATGATGATGATGATGATGATGATGAT 180
QY 181 AAATGAGACCTTGGAGAGACGACACCATCATATGCTGTAACCTGGCTCCAGAGATCTG 240
DB 181 AAATGAGACCTTGGAGAGACGACACCATCATATGCTGTAACCTGGCTCCAGAGATCTG 240
QY 241 CTGTATCTGACGACCTCCCTCCCTGATTCATGATGATGATGATGATGATGATGATGAT 300
DB 241 CTGTATCTGACGACCTCCCTCCCTGATTCATGATGATGATGATGATGATGATGATGAT 300
QY 301 TTGGAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 TTGGAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 ATCCCT 420
DB 361 ATCCCT 420
QY 421 TGGTTTTCATTTACAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
DB 421 TGGTTTTCATTTACAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 481 TCACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 541 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 541 TCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 601 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
DB 661 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720

QY 721 AGGCTAACCATCTCTGCTACTCCCTGCAATTTAGATGATGATGATGATGATGATGATGAT 780
DB 721 AGGCTAACCATCTCTGCTACTCCCTGCAATTTAGATGATGATGATGATGATGATGATGAT 780
QY 781 AGGCTAACCATCTCTGCTACTCCCTGCAATTTAGATGATGATGATGATGATGATGATGAT 840
DB 781 AGGCTAACCATCTCTGCTACTCCCTGCAATTTAGATGATGATGATGATGATGATGATGAT 840
QY 841 CATGAGCTTACATCT 900
DB 841 CATGAGCTTACATCT 900
QY 901 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 GTAAGGCGGACCTTACGACAGCAAGAAATTTAGTACTGCAACACCTTGA 1014
DB 961 GTAAGGCGGACCTTACGACAGCAAGAAATTTAGTACTGCAACACCTTGA 1014

RESULT 3

AAD26370 standard; cDNA; 1014 BP.

XX AAD26370:

XX 26-MAR-2002 (first entry)

XX Human G-protein coupled receptor 2 (GRC-2) cDNA.

XX Human; G-protein coupled receptor 2; cell proliferative disorder;
XX arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy;
XX Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
XX atherosclerosis; hypertension; myocardial infarction; peptic ulcer;
XX gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder;
XX acquired immune deficiency syndrome; inflammatory disorder; infection;
XX Addison's disease; allergy; Grave's disease; metabolic disorder; AIDS;
XX diabetes; obesity; osteoporosis; gene therapy; GRC-2; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..1014 /tag-a /product="Human GRC-2 protein"

XX NC0200187937-A2.

XX 22-NOV-2001.

XX 17-MAY-2001; 2001MO-US16285.

XX 18-MAY-2000; 2000US-205628P.

XX 22-MAY-2000; 2000US-206222P.

XX 25-MAY-2000; 2000US-207366P.

XX 02-JUN-2000; 2000US-208834P.

XX 02-JUN-2000; 2000US-208861P.

XX (INCY-) INCYTE GENOMICS INC.

XX Patterson C, Lu DAM, Thornton M, Lu Y, Tribouley CM, Gaul R;

XX Khan FA, Gandhi AR, Wajia NK, Nguyen DB, Yue H, Hafalia A;

XX Elliott VS, Lal P, Reddy R, Kallick DA, Tang TY, Au-Young J;

XX WPI; 2002-089844/12.

XX P-PSDB; AAE16171.

XX Novel G-protein coupled receptors and polynucleotides useful for diagnosis, treatment and prevention of disorders of cell proliferation, neurological, cardiovascular, metabolic disorders and viral infections

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DR P-PSDB; ABB83819.
 XX An isolated P2Y₁-like receptor polypeptide (HIPDM 000037) which can be
 PT used for the identification of agonists and antagonists which may be
 PS used to treat an immune or inflammatory disease.
 XX Claim 5; Page 28-29; 35pp; English.
 CC The invention relates to an isolated P2Y₁-like receptor polypeptide
 CC (ABB83819-ABB83819) which is also referred to in the specification as
 CC HIPDM 000037. An effective amount of a substance (agonist or
 CC antagonist) which modulates P2Y₁ receptor activity is useful to treat a
 CC subject having a disorder that is responsive to P2Y₁-like receptor
 CC modulation. The disorder is a disease of immunity or inflammation. The
 CC substance may also be used to manufacture a medicine for the treatment or
 CC prophylaxis of a disorder that is responsive to stimulation or modulation
 CC of P2Y₁-like receptor activity. Disorders which may be treated include
 CC colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome,
 CC gastroenteritis and colitis, inflammatory bowel syndrome, ulcerative
 CC colitis, rheumatoid arthritis, viral diseases, bacterial infections,
 CC autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic
 CC rhinitis, inflammatory pain and general inflammation such as tendonitis,
 CC polyarthritis or prostaticitis. The invention provides alternative
 CC substances for the treatment of immunological and inflammatory diseases.
 CC The present sequence is that the P2Y₁-like receptor variant encoding gene
 CC of the invention.
 XX
 SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other:

Query Match 99.8%; Score 1012.4; DB 24; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 2.1e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAGCCACCTAGATATTTAGCAATGCTTGTGATTTCCCGATATAGAGCTCT 60
 DB 1 ATGATGAGCCACCTAGATATTTAGCAATGCTTGTGATTTCCCGATATAGAGCTCT 60
 QY 61 TTGGAAATTCACCTGATGAAACATCCACATCAAGATGACCTACCTCTGTATTTAT 120
 DB 61 TTGGAAATTCACCTGATGAAACATCCACATCAAGATGACCTACCTCTGTATTTAT 120
 QY 121 GGCAATATCTCTCGTGGGATTTCCAGCAATGAGATGATGATTCACCTTATTTTC 180
 DB 121 GGCAATATCTCTCGTGGGATTTCCAGCAATGAGATGATGATTCACCTTATTTTC 180
 QY 181 AAAATGAGACCTTGGAGAGACGACCATATTAATGCTGAACCTGGCTGCACAGATCTG 240
 DB 181 AAAATGAGACCTTGGAGAGACGACCATATTAATGCTGAACCTGGCTGCACAGATCTG 240
 QY 241 CTGATCTGACAGCTCCCTCTCTGATTCATCTATGCGAGTGGGAAACCTGATC 300
 DB 241 CTGATCTGACAGCTCCCTCTCTGATTCATCTATGCGAGTGGGAAACCTGATC 300
 QY 301 TTGGAGATTCATGATGATTTATTCGCTTACCTTCCATTTCACTGTATAGAGC 360
 DB 301 TTGGAGATTCATGATGATTTATTCGCTTACCTTCCATTTCACTGTATAGAGC 360
 QY 361 ATCTCTCTCTACCTGTTTACGATCTTCGCTACTGTGATGATTCACCTATGAGC 420
 DB 361 ATCTCTCTCTACCTGTTTACGATCTTCGCTACTGTGATGATTCACCTATGAGC 420
 QY 421 TGTCTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGAT 480
 DB 421 TGTCTTTCATTCACAAAACCTGATGATGATGATGATGATGATGATGATGATGAT 480
 QY 481 TCAGTGTAGCTGATTCGATGATCTTCTGATCAGATCAACCAAGAGAGAGAGAG 540
 DB 481 TCAGTGTAGCTGATTCGATGATCTTCTGATCAGATCAACCAAGAGAGAGAGAG 540
 QY 541 TCAGCTGTCTGAGCTCAGAGTTCGATGATGATGATGATGATGATGATGATGATGAT 600
 DB 541 TCAGCTGTCTGAGCTCAGAGTTCGATGATGATGATGATGATGATGATGATGATGAT 600

QY 601 ATTTGACCTGCAACTACTTCTGCTCCCTGGTGTGATGATGACCTTCTATACACG 660
 DB 601 ATTTGACCTGCAACTACTTCTGCTCCCTGGTGTGATGATGACCTTCTATACACG 660
 QY 661 ATATTCACACCTGACACCTGATGATGATGATGATGATGATGATGATGATGATGAT 720
 DB 661 ATATTCACACCTGACACCTGATGATGATGATGATGATGATGATGATGATGATGAT 720
 QY 721 AGGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 DB 721 AGGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
 QY 781 AGGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 781 AGGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 841 CATGACCTTACATCTGTTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 841 CATGACCTTACATCTGTTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 900
 QY 901 CTATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 DB 901 CTATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 QY 961 GTAAGCGGAACTTGGAG 1014
 DB 961 GTAAGCGGAACTTGGAG 1014

RESULT 6
 ABRK1381
 ID ABRK1381 standard; DNA; 1014 BP.

ABRK1381;
 05-JUN-2002 (first entry)
 Human DNA encoding P2Y₁-like G protein-coupled receptor.

Human; ds; gene; P2Y₁-like G-protein-coupled receptor; GPCR;
 infection; pain; cancer; anorexia; bulimia; asthma; hypertension;
 central nervous system disease; acute heart failure; hypertension;
 urinary retention; osteoporosis; diabetes; angina pectoris;
 myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis;
 benign prostatic hyperplasia; psychosis; neurological disorder;
 dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder;
 Parkinson's disease; anxiety; schizophrenia; manic depression; delirium;
 dementia; severe mental retardation; Huntington's disease;
 Tourette's syndrome.

Homo sapiens.
 Key Location/Qualifiers
 CDS 1..1014
 FT /tag= a
 FT /product= "P2Y₁-like GPCR"

W0200214511-A2.
 21-FEB-2002.
 10-AUG-2001; 2001WO-EP09243.
 14-AUG-2000; 2000US-224989P.
 (FARB) BAYER AG.
 Ramakrishnan S;
 WPI: 2002-257607/30.
 DR P-PSDB; AAU77600.
 Novel human P2Y₁-like G protein-coupled receptor polypeptide which can

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PT be regulated for treating infection, pain, cancer, diabetes, anorexia,
 PT asthma, hypertension, neurological disorder and dyskinesia
 XX
 PS Claim 1: Fig 5, 118pp: English.

XX The invention relates to a purified human P2Y1-like G protein-coupled
 CC receptor (GPCR) polypeptide and the nucleic acids encoding it
 CC (including 5' and 3' sequences, promoters, fragments, variants, or a
 CC sequence encoding a protein at least 50% identical to the GPCR).
 CC Also included are an expression vector comprising the nucleic acid,
 CC a host cell containing the vector and the identification of modulators of
 CC the GPCR especially those that reduce the activity of the GPCR.
 CC The nucleic acid is useful for detecting a polynucleotide encoding
 CC the GPCR in a biological sample. The GPCR and nucleic acid are useful for
 CC screening for agents which decrease the activity of the GPCR and
 CC for modulators of the GPCR. The modulator or agent useful for modulating
 CC the activity of P2Y1-like G protein-coupled receptor in a disease such as
 CC bacterial, fungal, protozoan, and viral infection, pain, cancer,
 CC anorexia, bulimia, asthma, central nervous system (CNS) disease, acute
 CC heart failure, hypotension, hypertension, urinary retention, ulcer,
 CC osteoporosis, diabetes, angina pectoris, myocardial infarction, ulcer,
 CC inflammation, allergy, multiple sclerosis, benign prostatic hypertrophy,
 CC psychotropic and neurological disorders, dyskinesias, HIV virus infection
 CC (human immunodeficiency virus), CNS disorders such as Parkinson's
 CC disease, anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation, Huntington's disease and Tourette's syndrome.
 CC The present sequence encodes the P2Y1-like GPCR of the invention.
 XX
 XX Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;

Query Match 99.8%; Score 1012.4; DB 24; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 2,1e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAGCCACTAGACTATTTAGCAAAATGCTTCGATTCCCGCATATGACAGCTGCT 60
 DB 1 ATGATGAGCCACTAGACTATTTAGCAAAATGCTTCGATTCCCGCATATGACAGCTGCT 60
 QY 61 TTGGAAATTTGCACTATGAAAACATCCCAATGAGTACACTCTCCCTGTTATTTAT 120
 DB 61 TTGGAAATTTGCACTATGAAAACATCCCAATGAGTACACTCTCCCTGTTATTTAT 120
 QY 121 GGCATATCTTCCTCGTGGGATTTCCAGGCAATGAGTACACTCTCTCAATTTTC 180
 DB 121 GGCATATCTTCCTCGTGGGATTTCCAGGCAATGAGTACACTCTCTCAATTTTC 180
 QY 181 AAAATGAGACCTTGAAGAGACAGCACCATCATTTATGCTGAACCTGGCTGCACAGATCTG 240
 DB 181 AAAATGAGACCTTGAAGAGAGACAGCACCATCATTTATGCTGAACCTGGCTGCACAGATCTG 240
 QY 241 CTGTATCTGACAGCCTCCCTCTCGATTCACACTATGAGCCAGTGGCGAAAACCTGGATC 300
 DB 241 CTGTATCTGACAGCCTCCCTCTCGATTCACACTATGAGCCAGTGGCGAAAACCTGGATC 300
 QY 301 TTGGAGATTTATGTAAGTATTAATCCGCTGAGCTTCATTTCAACCTGTATATAGAGC 360
 DB 301 TTGGAGATTTATGTAAGTATTAATCCGCTGAGCTTCATTTCAACCTGTATATAGAGC 360
 QY 361 ATCCCTTCCTCAGCTGTTTACAGATCTTCGCTAGCTGTGTGATTCACCAATGAGC 420
 DB 361 ATCCCTTCCTCAGCTGTTTACAGATCTTCGCTAGCTGTGTGATTCACCAATGAGC 420
 QY 421 TCGTTTTCATTCACAAAACCTGATGTGAGCTGTGCTGTGTGTGTGATTCATT 480
 DB 421 TCGTTTTCATTCACAAAACCTGATGTGAGCTGTGCTGTGTGTGTGATTCATT 480
 QY 481 TCACCTGTAGCTGTCAATTCGAGTACCTTTTATGATCAGATCAACACAGAGACCAAGAGA 540
 DB 481 TCACCTGTAGCTGTCAATTCGAGTACCTTTTATGATCAGATCAACACAGAGACCAAGAGA 540
 QY 541 TCAGCTGTCTCGACCTCAACAGTGTGATGATCAATCTATTAAGTGGTCAACCTGA 600
 DB 541 TCAGCTGTCTCGACCTCAACAGTGTGATGATCAATCTATTAAGTGGTCAACCTGA 600

QY 601 ATTATGACCTGCAACTCTTTCTGCGCCCTCCCTGGTATGATGACACTTTGCTATACAGC 660
 DB 601 ATTATGACCTGCAACTCTTTCTGCGCCCTCCCTGGTATGATGACACTTTGCTATACAGC 660
 QY 661 ATTATGACCTGCAACTCTTTCTGCGCCCTCCCTGGTATGATGACACTTTGCTATACAGC 720
 DB 661 ATTATGACCTGCAACTCTTTCTGCGCCCTCCCTGGTATGATGACACTTTGCTATACAGC 720
 QY 721 AGGCTATTCAGTCTGCTACTCTGCAATTTTACGATGATGATGATGATGATGATGATGAT 780
 DB 721 AGGCTATTCAGTCTGCTACTCTGCAATTTTACGATGATGATGATGATGATGATGATGAT 780
 QY 781 AGGCTATTCAGTCTGCTACTCTGCAATTTTACGATGATGATGATGATGATGATGATGAT 840
 DB 781 AGGCTATTCAGTCTGCTACTCTGCAATTTTACGATGATGATGATGATGATGATGATGAT 840
 QY 841 CATGAGCTTACATCTGCTTCTAGACCATTTAGCTGCTGTAACACCTTTGGTAACTGTTA 900
 DB 841 CATGAGCTTACATCTGCTTCTAGACCATTTAGCTGCTGTAACACCTTTGGTAACTGTTA 900
 QY 901 CTATATGT 960
 DB 901 CTATATGT 960
 QY 961 GTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
 DB 961 GTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014

RESULT 7
 AAK98323
 ID AAK98323 standard; cDNA; 1014 BP.

XX AAK98323;
 AC 30-APR-2002 (first entry)
 DT XX
 DE Human purinergic-related G-protein coupled receptor (GPCR) cDNA sequence.
 XX
 XX Human; chromosome 13; purinergic GPCR; G-protein coupled receptor;
 KW signal transduction; human protease; GPCR disorder; gene therapy;
 KW transgenic animal; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 1..1014
 FT /*tag= a
 FT /product= "G-protein coupled receptor"
 XX
 XX WO200187980-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001MO-US15957.
 XX
 XX 18-MAY-2000; 2000US-205196P.
 PR 08-AUG-2000; 2000US-0634656.
 XX
 PA (APPL-) APPLERA CORP.
 XX
 XX Wei M, Zhao Q, Cravchik A, Di Francesco V, Beasley EM;
 PT WPI; 2002-075312/10.
 DR P-PSDB; AA014027.
 XX
 XX Novel isolated G-protein coupled receptor peptide useful for treating
 PT disorder characterized by absence of, in appropriate or unwanted
 PT expression of the receptor protein, and as immunogens to raise
 PT antibodies -
 XX
 PS Claim 23; Fig 1; 64pp: English.

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XX The present specifically claimed human cDNA sequence (located on
 CC chromosome 13) encodes a purinergic-related G-protein coupled receptor
 CC (GPCR) of the invention. GPCRs constitute a major class of proteins
 CC responsible for signal transduction within a cell. Upon binding of a
 CC ligand to the extracellular portion of a GPCR, a signal is transduced
 CC resulting in a biological or physiological change within the cell. The
 CC GPCR proteins can be divided into five families, family I contains the
 CC purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are
 CC characterised by their selective responsiveness towards ATP and its
 CC analogues, some also respond to UTP. The invention comprises a human
 CC G-protein coupled receptor protein and encoding nucleic acids. The GPCR
 CC protein and nucleic acids of the invention are useful in the treatment of
 CC a disease or condition mediated by a human protease. The GPCR protein of
 CC the invention is useful for: the development/identification of
 CC therapeutic proteins; assays designed to quantitatively determine levels
 CC of the protein in biological fluids; identifying compounds which modulate
 CC the activity of the GPCR, or the interaction of the GPCR and a molecule
 CC with which it normally interacts; and treating a disorder characterised
 CC by an absence of, or inappropriate expression of the GPCR protein. The
 CC GPCR nucleic acids of the invention are useful in diagnostic assays to
 CC identify changes in the GPCR nucleic acid that lead to pathology.
 CC Controlling GPCR expression; and in gene therapy to treat patients with
 CC aberrant GPCR gene expression. The GPCR nucleic acids can also be used in
 CC the production of transgenic animals.
 XX
 SQ Sequence 1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;
 Query Match 99.8%; Score 1012.4; DB 24; Length 1014;
 Best Local Similarity 99.9%; Pred. No. 2.1e-288;
 Matches 1013; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAGCCACTAGACTATTAGCAATGCTTCGATTTCCCGCATATGAGCTGCT 60
 DB 1 ATGATGAGCCACTAGACTATTAGCAATGCTTCGATTTCCCGCATATGAGCTGCT 60
 QY 61 TTTGGAATTTGACATGATGAAACATCCACATCAAGATGACATCCCTGTTATTAT 120
 DB 61 TTTGGAATTTGACATGATGAAACATCCACATCAAGATGACATCCCTGTTATTAT 120
 QY 121 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAATGATGATTCATTTAT 180
 DB 121 GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAATGATGATTCATTTAT 180
 QY 181 AAAATGAGACCTTGGAGAGACGACACATCATATGCTGAACTGGCTGACAAAGATCTG 240
 DB 181 AAAATGAGACCTTGGAGAGACGACACATCATATGCTGAACTGGCTGACAAAGATCTG 240
 QY 241 CTGTATCTGACGACCTCCCTCTGATTCATCTATGACGAGTGGCGAAACTGGATC 300
 DB 241 CTGTATCTGACGACCTCCCTCTGATTCATCTATGACGAGTGGCGAAACTGGATC 300
 QY 301 TTTGAGATTTCTATGTAAGTTATCCGCTTACGCTTCATTTCAACCTGTATAGAGC 360
 DB 301 TTTGAGATTTCTATGTAAGTTATCCGCTTACGCTTCATTTCAACCTGTATAGAGC 360
 QY 361 ATCCCTTCTGCTACCTGTTTACAGATCTTCCGCTACTGTTGATCATTCACCAAGAGC 420
 DB 361 ATCCCTTCTGCTACCTGTTTACAGATCTTCCGCTACTGTTGATCATTCACCAAGAGC 420
 QY 421 TGCTTTTCATTCACAAACTGATGATGAGTGTGACCTGTGCTGTGGTGGATCAT 480
 DB 421 TGCTTTTCATTCACAAACTGATGATGAGTGTGACCTGTGCTGTGGTGGATCAT 480
 QY 481 TCACGTGATGCTCATTTCCGATGAGCTTCTTATCATCATCAACCAAGAGACAGAGA 540
 DB 481 TCACGTGATGCTCATTTCCGATGAGCTTCTTATCATCATCAACCAAGAGACAGAGA 540
 QY 541 TCAGCTGTCTGAGCTCACAGCTGGAGTGAATCAATCTTAAGTGTGTAACCTGA 600
 DB 541 TCAGCTGTCTGAGCTCACAGCTGGAGTGAATCAATCTTAAGTGTGTAACCTGA 600
 QY 601 ATTTCAGTGCAGACTTCTTCTGCTCCCTGTGTGATATGACACTTCTCTATACAGC 660

DB 601 ATTTCAGTGCAGACTTCTTCTGCTCCCTGTGTGATATGACACTTCTCTATACAGC 660
 QY 661 ATTTCAGTGCAGACTTCTTCTGCTCCCTGTGTGATATGACACTTCTCTATACAGC 720
 DB 661 ATTTCAGTGCAGACTTCTTCTGCTCCCTGTGTGATATGACACTTCTCTATACAGC 720
 QY 721 AGGCTAACATCTCTACTCTCCCTTCATTTAGTATGTTTATACCTTCATATCTTG 780
 DB 721 AGGCTAACATCTCTACTCTCCCTTCATTTAGTATGTTTATACCTTCATATCTTG 780
 QY 781 AGGCTAACATCTCTACTCTCCCTTCATTTAGTATGTTTATACCTTCATATCTTG 840
 DB 781 AGGCTAACATCTCTACTCTCCCTTCATTTAGTATGTTTATACCTTCATATCTTG 840
 QY 841 CATGAAGCTTATGTTTCTGACCATTAAGTGTCTGTAACACCTTGTGTAACCTGTA 900
 DB 841 CATGAAGCTTATGTTTCTGACCATTAAGTGTCTGTAACACCTTGTGTAACCTGTA 900
 QY 901 CTATATGTGTGTGTCAGACACACTTTCAGAGGCTGTCTGTCAACAGTAGATGCAAA 960
 DB 901 CTATATGTGTGTGTCAGACACACTTTCAGAGGCTGTCTGTCTCAACAGTAGATGCAAA 960
 QY 961 GTAAGCGGGAACCTTGAGCAACGAAAGAAATTAAGTACTCAAAACACCTTGA 1014
 DB 961 GTAAGCGGGAACCTTGAGCAACGAAAGAAATTAAGTACTCAAAACACCTTGA 1014

RESULT 8
 ABL56197
 ID ABL56197 standard; cDNA; 1288 BP.
 XX
 AC ABL56197;
 DT 05-JUL-2002 (first entry)
 DE Human P2Y1-11 encoding cDNA.
 XX
 KW Human, P2Y1-11, chromosome 13; G protein-coupled; receptor;
 KW gene therapy; thyroid; gene; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 18..1031
 FT /tag a
 FT /product "P2Y1-like purine receptor"
 XX
 DE10046970-A1.
 XX
 PD 11-APR-2002.
 XX
 PF 22-SEP-2000; 2000DE-1046970.
 XX
 PR 22-SEP-2000; 2000DE-1046970.
 XX
 PA (BRUE/) BRUESS M.
 PA (BOEN/) BOENISCH H.
 XX
 PI Brues M., Boenisch H;
 DR WPI: 2002-353329/39.
 DR P-PDB: ABB79438.
 XX
 PT New human P2Y11 gene, useful for treatment and diagnosis of associated
 PT diseases, and related proteins, antibodies and modulators, encodes G
 PT protein-coupled receptor
 XX
 PS Claim 5; Page 3; 5pp; German.
 CC
 CC The invention relates to the human P2Y11 gene (I), including its 5' and
 CC 3' untranslated regions, located on chromosome 13 and encoding a G
 CC protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies

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8309 ATGAATGAGCCACTAATATTTAGCAAAATGCTTGTATTCCTCCGATTTATGAGAGCTGCT 8368
OY TTTGGAATTTGCACTGATGATGAAATATCCCAATGATGACATCCCTGATATTTAT 120
Db TTTGGAATTTGCACTGATGATGAAATATCCCAATGATGACATCCCTGATATTTAT 8428
OY TTTGGAATTTGCACTGATGATGAAATATCCCAATGATGACATCCCTGATATTTAT 180
Db TTTGGAATTTGCACTGATGATGAAATATCCCAATGATGACATCCCTGATATTTAT 8488
OY TTTGGAATTTGCACTGATGATGAAATATCCCAATGATGACATCCCTGATATTTAT 240
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Db TTTGGAATTTGCACTGATGATGAAATATCCCAATGATGACATCCCTGATATTTAT 8848
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OY TTTGGAATTTGCACTGATGATGAAATATCCCAATGATGACATCCCTGATATTTAT 1014
Db TTTGGAATTTGCACTGATGATGAAATATCCCAATGATGACATCCCTGATATTTAT 9322

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RESULT 11
 AAS08362
 ID AAS08362 standard; cDNA; 1729 BP.
 XX
 AAS08362;

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XX 26-SEP-2001 (first entry)
DT Human cDNA encoding G-protein coupled receptor, GPCR 39404.
XX
DE Human; G-protein coupled receptor; GPCR; 39404; immunogen; antibody;
KW Good pasture's syndrome; viral hepatitis; Alzheimer's disease; lymphoma;
KW Heymann nephritis; Paget's disease; Crohn's disease; endometriosis;
KW systemic lupus erythematosus; actinic keratosis; myocarditis;
KW Kawasaki syndrome; DiGeorge syndrome; peripheral B-cell neoplasia;
KW inflammations; teratoma; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 294..1307
FT /tag="a
FT /product="Protein 39404"
XX
PD WO200149847-A2.
XX
XX 12-JUL-2001.
XX
XX 22-DEC-2000; 2000MO-US35309.
XX
XX 30-DEC-1999; 99US-0475790.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Glucksmann MA, White D;
XX
XX WPI: 2001-432880/46.
XX P-PSDB; AA004584.
XX
XX Novel isolated 26904, 38911 and 39404 polypeptides which are seven
XX transmembrane proteins belonging to superfamily of G-protein-coupled
XX PT receptors, useful for treating disorders of spleen, lung, liver, brain
XX PT and kidney -
XX
XX Claim 2; Fig 1; 164pp; English.
XX
XX The sequence encodes a novel human seven transmembrane domain
XX CC protein belonging to the G-protein coupled receptor (GPCR) superfamily,
XX CC protein 39404. The receptor is useful in drug screening assays, to
XX CC identify compounds that modulate receptor activity and/or interact with
XX CC the receptor, and for producing antibodies specific for the receptor, its
XX CC regions or fragments. The receptor is useful for treating/diagnosing a
XX CC 26904, 38911 and 39404 protein-associated disorder characterised by
XX CC aberrant expression or activity of the protein, for monitoring
XX CC therapeutic effect during clinical trials and other treatment, as bait
XX CC proteins in a two-hybrid or three-hybrid assay, and in pharmacogenomic
XX CC analysis. The proteins and nucleic acids encoding them are useful for
XX CC diagnosis and treatment of disorders selected from disorders of the
XX CC spleen, lung such as Good pasture's syndrome, liver such as viral
XX CC hepatitis, brain such as Alzheimer's disease, haematopoietic stem cells
XX CC such as lymphoma, kidney such as Heymann nephritis, bone such as Paget's
XX CC disease, colon such as Crohn's disease, uterus and endometrium such as
XX CC endometriosis, T-cell disorders such as systemic lupus erythematosus,
XX CC diseases of the skin such as actinic keratosis, disorders of the heart
XX CC such as myocarditis, disorders involving blood vessels such as Kawasaki
XX CC syndrome, disorders involving the thymus such as DiGeorge syndrome,
XX CC disorders involving B-cells such as peripheral B-cell neoplasia,
XX CC disorders of the breast such as inflammations, and disorders involving
XX CC the testis and epididymis such as teratoma. Numerous examples of
XX CC each type of disorder are given in the specification.
XX
XX Sequence 1729 BP; 461 A; 403 C; 302 G; 563 T; 0 other;
XX
XX Query Match 99.7%; Score 1010.8; DB 22; Length 1729;
XX Best local Similarity 99.8%; Pred. No. 8.2e-288;
XX Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 ATGAATGAGCCACTAATATTTAGCAAAATGCTTGTATTCCTCCGATTTATGAGAGCTGCT 60

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Db      294 ATGAAGAGACCTAGACCTTTAGCAAAAGCTTCTATTTCCCGGATTTATGACGCTGCT 353
QY      61 TTTGAAATTCGACTGATGAAAACATCCACTCAAGATGACATACCCCGTATTTAT 120
Db      354 TTTGAAATTCGACTGATGAAAACATCCACTCAAGATGACATACCCCGTATTTAT 413
QY      121 GGCATTATCTCTCGTGGGATTTCCAGGCAATGACATGATGATATTCATTTTC 180
Db      414 GGCATTATCTCTCGTGGGATTTCCAGGCAATGACATGATGATATTCATTTTC 473
QY      181 AAAATGAGACCTTGGAAAGACAGACCATCATATATGCTGAACCTGGCCTGACAGATCTG 240
Db      474 AAAATGAGACCTTGGAAAGACAGACCATCATATATGCTGAACCTGGCCTGACAGATCTG 533
QY      241 CTGATATCGACAGCCCGCCCTCCGATTCACACATGATGCAATGCGATGGCAAAATGTGATC 300
Db      534 CTGATATCGACAGCCCGCCCTCCGATTCACACATGATGCAATGCGATGGCAAAATGTGATC 593
QY      301 TTTGAGATTTCAATGTTAAGTTATTCGCTTCAGCTTCATTCATTCACCTGATATGACAGC 360
Db      594 TTTGAGATTTCAATGTTAAGTTATTCGCTTCAGCTTCATTCATTCACCTGATATGACAGC 653
QY      361 ATCCTCTTCCACACTGTTTCAGACATCTCCGCTACTGCTGATCATTTCAACCCATGAC 420
Db      654 ATCCTCTTCCACACTGTTTCAGACATCTCCGCTACTGCTGATCATTTCAACCCATGAC 713
QY      421 TGCCTTTCCATTCACAAAACCTCGATGTCAGTTGTAGCTGCTGCTGTGTGTGATCAT 480
Db      714 TGCCTTTCCATTCACAAAACCTCGATGTCAGTTGTAGCTGCTGCTGTGTGTGATCAT 773
QY      481 TCACTGCTAGCTGCTGATTCGATGACCTCTGTGATCATCAACCAACAGAACCAAGA 540
Db      774 TCACTGCTAGCTGCTGATTCGATGACCTCTGTGATCATCAACCAACAGAACCAAGA 833
QY      541 TCAAGCTGTCTCGACCTCACCAGTTCGAGATGACATCACTATTAAGTGTACAACTA 600
Db      834 TCAAGCTGTCTCGACCTCACCAGTTCGAGATGACATCACTATTAAGTGTACAACTA 893
QY      601 ATTTTGACTGCACTACTTTCGCTCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db      894 ATTTTGACTGCACTACTTTCGCTCCCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 953
QY      661 ATTAATCAGACTGACCACTGACATGACATGACATGACATGACATGACATGACATGACAT 720
Db      954 ATTAATCAGACTGACCACTGACATGACATGACATGACATGACATGACATGACATGACAT 1013
QY      721 AGGCTAACACTTCTGCTACTCTCTGCAATTTTACATGATTTTACCTTCCATATCTTG 780
Db      1014 AGGCTAACACTTCTGCTACTCTCTGCAATTTTACATGATTTTACCTTCCATATCTTG 1073
QY      781 AGGCTCAATGGATGCAATCTCGCCTGCTTCAATGATTTTCCATTTGAGATCAATC 840
Db      1074 AGGCTCAATGGATGCAATCTCGCCTGCTTCAATGATTTTCCATTTGAGATCAATC 1133
QY      841 CATGACACTTTCATCGTTTCTAGACATTTAGCTGTGACACACTTGGTGAATCTGTTA 900
Db      1134 CATGACACTTTCATCGTTTCTAGACATTTAGCTGTGACACACTTGGTGAATCTGTTA 1193
QY      901 CTATATGTGTGTGTGTCAGAGCACTTTCAGCAGGCTGTCTCAACAGTGAATGCAAA 960
Db      1194 CTATATGTGTGTGTGTCAGAGCACTTTCAGCAGGCTGTCTCAACAGTGAATGCAAA 1253
QY      961 GTAAGCGGGAACCTTGAAGCAAGCAAAATTTAGTTACTCAAAACACCTTTGA 1014
Db      1254 GTAAGCGGGAACCTTGAAGCAAGCAAAATTTAGTTACTCAAAACACCTTTGA 1307

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RESULT 12
 ABV24026
 ID ABV24026 standard; cDNA; 1729 BP.
 XX
 AC ABV24026;

```

XX      16-SEP-2002 (first entry)
DE      Human prostate expression marker cDNA 24017.
KW      Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
        pharmacogenomic marker; gene; ss.
OS      Homo sapiens.
PN      NO200160860-A2.
PD      23-AUG-2001.
PF      20-FEB-2001; 2001MO-US05171.
PR      17-FEB-2000; 2000US-183319P.
PR      16-MAR-2000; 2000US-189862P.
PR      25-MAY-2000; 2000US-207454P.
PR      09-JUN-2000; 2000US-211314P.
PR      18-JUL-2000; 2000US-219007P.
PR      13-DEC-2000; 2000US-255281P.
XX
XX      (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC.
PI      Schlegel R, Endege WO, Monahan JE.
XX      WPI; 2001-662795/76.
XX
XX      Novel isolated nucleic acid molecule associated with cancerous state of
PT      prostate cells and correlating with presence of prostate cancer, useful
PT      for detecting presence of prostate cancer, stage of prostate cancer -
XX      Claim 1; Page 4453-4454; 11750pp; English.
XX
XX      The invention relates to an isolated nucleic acid molecule (I) comprising
CC      a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC      specification or its complement. (I) is useful for:
CC      (a) assessing whether a patient is afflicted with prostate cancer;
CC      (b) monitoring the progression of prostate cancer in a patient;
CC      (c) assessing the efficacy of a test compound to inhibit prostate
CC      cancer in a patient;
CC      (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC      in a patient;
CC      (e) selecting a composition for inhibiting prostate cancer in a patient;
CC      (f) assessing the prostate cell carcinogenic potential of a compound;
CC      (g) determining whether prostate cancer has metastasized in a patient;
CC      (h) assessing the aggressiveness or indolence of prostate cancer in a
CC      patient;
CC      (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ      Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;
Query Match          99.7%; Score 1010.8; DB 23; Length 1729;
Best Local Similarity 99.8%; Pred. No. 8.2e-288;
Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 ATGAATGAGCAGCAGCTATTTAGCAAAAGCTTCTGATTTCCCGGATTTATGACGCTGCT 60
Db      294 ATGAATGAGCAGCAGCTATTTAGCAAAAGCTTCTGATTTCCCGGATTTATGACGCTGCT 353
QY      61 TTTGAAATTCGACTGATGAAAACATCCACTCAAGATGACATACCCCGTATTTAT 120
Db      354 TTTGAAATTCGACTGATGAAAACATCCACTCAAGATGACATACCCCGTATTTAT 413
QY      121 GGCATTATCTCTCGTGGGATTTCCAGGCAATGACATGATGATATTCATTTTC 180
Db      414 GGCATTATCTCTCGTGGGATTTCCAGGCAATGACATGATGATATTCATTTTC 473
QY      181 AAAATGAGACCTTGGAAAGACAGACCATCATATATGCTGAACCTGGCCTGACAGATCTG 240
Db      474 AAAATGAGACCTTGGAAAGACAGACCATCATATATGCTGAACCTGGCCTGACAGATCTG 533

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QY 241 CTGTATCTGACAGCCCTCCCTTCCTGATTCATCTATGAGCAGTGGCGAAATCTGATC 300
 |||||||
 Db 534 CTGTATCTGACAGCCCTCCCTTCCTGATTCATCTATGAGCAGTGGCGAAATCTGATC 593
 |||||||
 QY 301 TTGGAGATTTCATGTGTAGTTTATCCGCTTCAGCTTCATTTCAACTGTATAGAGC 360
 |||||||
 Db 594 TTGGAGATTTCATGTGTAGTTTATCCGCTTCAGCTTCATTTCAACTGTATAGAGC 653
 |||||||
 QY 361 ATCCCTCTCCCTGACAGCTTCGATTCCTCCGCTTCAGCTTCATTTCAACTGTATAGAGC 420
 |||||||
 Db 654 ATCCCTCTCCCTGACAGCTTCGATTCCTCCGCTTCAGCTTCATTTCAACTGTATAGAGC 713
 |||||||
 QY 421 TGCCTTTCCATTCACAAAATCTCGATGTGAGTTGATTCAGCTTCGATGTGAGTTGATTCAT 480
 |||||||
 Db 714 TGCCTTTCCATTCACAAAATCTCGATGTGAGTTGATTCAGCTTCGATGTGAGTTGATTCAT 773
 |||||||
 QY 481 TCAGCTGTAGCTTCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 540
 |||||||
 Db 774 TCAGCTGTAGCTTCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 833
 |||||||
 QY 541 TCAGCTGTAGCTTCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 600
 |||||||
 Db 834 TCAGCTGTAGCTTCATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 893
 |||||||
 QY 601 ATTTGATCTGCAACTACTTCTGCTCCCTCCCTGCTGATTCGATTCGATTCGATTCGATTCGATTC 660
 |||||||
 Db 894 ATTTGATCTGCAACTACTTCTGCTCCCTCCCTGCTGATTCGATTCGATTCGATTCGATTCGATTC 953
 |||||||
 QY 661 ATTTGATCTGCAACTACTTCTGCTCCCTCCCTGCTGATTCGATTCGATTCGATTCGATTCGATTC 720
 |||||||
 Db 954 ATTTGATCTGCAACTACTTCTGCTCCCTCCCTGCTGATTCGATTCGATTCGATTCGATTCGATTC 1013
 |||||||
 QY 721 AGGCTAACCACTTCTGCTACTCTTCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 780
 |||||||
 Db 1014 AGGCTAACCACTTCTGCTACTCTTCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 1073
 |||||||
 QY 781 AGGCTAACCACTTCTGCTACTCTTCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 840
 |||||||
 Db 1074 AGGCTAACCACTTCTGCTACTCTTCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 1133
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 QY 841 CATGAGCTTACATCGTTTCTAGACCACTTACGCTGCTGATTCGATTCGATTCGATTCGATTCGATTC 900
 |||||||
 Db 1134 CATGAGCTTACATCGTTTCTAGACCACTTACGCTGCTGATTCGATTCGATTCGATTCGATTCGATTC 1193
 |||||||
 QY 901 CTATATGTGTGTGTCAGCAGCACTTTCAGCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 |||||||
 Db 1194 CTATATGTGTGTGTCAGCAGCACTTTCAGCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1253
 |||||||
 QY 961 GTTAAGCGGGAACCTTGAAGCAAGCAAAATTAAGTTACTCAACCAACCTTGA 1014
 |||||||
 Db 1254 GTTAAGCGGGAACCTTGAAGCAAGCAAAATTAAGTTACTCAACCAACCTTGA 1307
 |||||||

RESULT 13

ABV25767 standard; cDNA: 1729 BP.

ID ABV25767;

AC ABV25767;

DF 16-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 25758.

KM Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-0505171.

XX 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 PI WPL; 2001-662795/76.
 DR
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 PS Claim 1; Page 5175-5176; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;
 Query Match 99.7%; Score 1010.8; DB 23; Length 1729;
 Best Local Similarity 99.8%; Pred. No. 8.2e-288;
 Matches 1012; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGAATGAGCCACTAGACTTATTTAGCAAAAGCTTGTGATTTCCCGCATTTAGAGCTGCT 60
 |||||||
 Db 294 ATGAATGAGCCACTAGACTTATTTAGCAAAAGCTTGTGATTTCCCGCATTTAGAGAGCTGCT 353
 |||||||
 QY 61 TTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTGTTATTTAT 120
 |||||||
 Db 354 TTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTGTTATTTAT 413
 |||||||
 QY 121 GGCATTAATCTTCTGCTGCGATTTCCAGGCAATGCAATGATGATTCATTAATTTTC 180
 |||||||
 Db 414 GGCATTAATCTTCTGCTGCGATTTCCAGGCAATGCAATGATGATTCATTAATTTTC 473
 |||||||
 QY 181 AAATGAGACCTTGAAGAGACAGCAGCATATTTAGTGAACCTGCGCTCAGAGATCTG 240
 |||||||
 Db 474 AAATGAGACCTTGAAGAGACAGCAGCATATTTAGTGAACCTGCGCTCAGAGATCTG 533
 |||||||
 QY 241 CTGTATCTGACAGCCCTCCCTTCCTGATTCATCTATGAGCAGTGGCGAAATCTGATC 300
 |||||||
 Db 534 CTGTATCTGACAGCCCTCCCTTCCTGATTCATCTATGAGCAGTGGCGAAATCTGATC 593
 |||||||
 QY 301 TTGGAGATTTCATGTGTAGTTTATCCGCTTCAGCTTCATTTCAACTGTATAGAGC 360
 |||||||
 Db 594 TTGGAGATTTCATGTGTAGTTTATCCGCTTCAGCTTCATTTCAACTGTATAGAGC 653
 |||||||
 QY 361 ATCCCTCTCCCTGACAGCTTCGATTCCTCCGCTTCAGCTTCATTTCAACTGTATAGAGC 420
 |||||||
 Db 654 ATCCCTCTCCCTGACAGCTTCGATTCCTCCGCTTCAGCTTCATTTCAACTGTATAGAGC 713
 |||||||
 QY 421 TGCCTTTCCATTCACAAAATCTCGATGTGAGTTGATTCAGCTTCGATGTGAGTTGATTCAT 480
 |||||||
 Db 714 TGCCTTTCCATTCACAAAATCTCGATGTGAGTTGATTCAGCTTCGATGTGAGTTGATTCAT 773
 |||||||

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Db 954 ATTATCAACTCTGACCCATGAGTGCNAAGTACAGCTGCTTAAAGCAGAAAGCAGCA 1013
 Qy 721 AGGCTAACCATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 780
 Db 1014 AGGCTAACCATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 1073
 Qy 781 AGGCTAACCATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 840
 Db 1074 AGGCTAACCATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 1133
 Qy 841 CATGAAGCTTACATGCTTCTAGACCATTAAGTCTGTCTGACACCTTTGGTAACTCTTGA 900
 Db 1134 CATGAAGCTTACATGCTTCTAGACCATTAAGTCTGTCTGACACCTTTGGTAACTCTTGA 1193
 Qy 901 CTATATGTTGTTGCTGACGACCAACTTTCAGACGCTGTCTGCTCAACAGTGAAGTCAAA 960
 Db 1194 CTATATGTTGTTGCTGACGACCAACTTTCAGACGCTGTCTGCTCAACAGTGAAGTCAAA 1253
 Qy 961 GTAAAGGGAACCTTGAAGCAAGCAAAATTAAGTACTCAAAACACCTTGA 1014
 Db 1254 GTAAAGGGAACCTTGAAGCAAGCAAAATTAAGTACTCAAAACACCTTGA 1307

RESULT 15
 ABV30024
 ID ABV30024 standard; cDNA; 1729 BP.
 XX
 AC ABV30024;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 30015.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 OS Homo sapiens.
 OS
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-0050171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR MPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 XX Claim 1; Page 6487-6488; 11750pp; English.
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;

CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SO Sequence 1729 BP; 461 A; 401 C; 302 G; 548 T; 17 other;

Query Match 99.7%; Score 1010.8; DB 23; Length 1729;
 Best Local Similarity 99.8%; Pred. No. 8.2e-288;
 Matches 1012; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTGTGATTTCCGATATAGCAGCTGCT 60
 Db 294 ATGAATGAGCCACTAGACTATTAGCAAAATGCTTGTGATTTCCGATATAGCAGCTGCT 353
 Qy 61 TTTGGAAATTTGACATGATGAAAACATCCCATCAAGATGACATCTCCCTGTATTAT 120
 Db 354 TTTGGAAATTTGACATGATGAAAACATCCCATCAAGATGACATCTCCCTGTATTAT 413
 Qy 121 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGAGATGATATCCACTACATTTTC 180
 Db 414 GGCATTATCTTCTCGTGGGATTTCCAGGCAATGAGATGATATCCACTACATTTTC 473
 Qy 181 AAAATGAGACTTGGAAAGAGACAGACCATATTAGCTGAACTGGCTGACAGATCTG 240
 Db 474 AAAATGAGACTTGGAAAGAGACAGACCATATTAGCTGAACTGGCTGACAGATCTG 533
 Qy 241 CTGTATCTGACAGCCTCCCTCTCTGATTCATCTACTATGACAGTGGCAAACTGGATC 300
 Db 534 CTGTATCTGACAGCCTCCCTCTCTGATTCATCTACTATGACAGTGGCAAACTGGATC 593
 Qy 301 TTTGGAGATTTATGTTGATGATTTATCCGCTTCACTTCAATTCACCTGATATACAG 360
 Db 594 TTTGGAGATTTATGTTGATGATTTATCCGCTTCACTTCAATTCACCTGATATACAG 653
 Qy 361 ATCCCTTCTCCTACCTGTTTCAAGCATCTTCCGCTACTGCTGATTCATTCACCAATGAGC 420
 Db 654 ATCCCTTCTCCTACCTGTTTCAAGCATCTTCCGCTACTGCTGATTCATTCACCAATGAGC 713
 Qy 421 TGCTTTTCCATTACAAAACCTGATGTGACATTTGACCTGTGCTGTGATGATCATT 480
 Db 714 TGCTTTTCCATTACAAAACCTGATGTGACATTTGACCTGTGCTGTGATGATCATT 773
 Qy 481 TCACGTGATGCTGCTCAATTCGATGACCTTCTTATACATCAACCAAGAGACCAAGCA 540
 Db 774 TCACGTGATGCTGCTCAATTCGATGACCTTCTTATACATCAACCAAGAGACCAAGCA 833
 Qy 541 TCAGCGCTGCTGACCTGACCACTGATGATGATGATGATGATGATGATGATGATGATG 600
 Db 834 TCAGCGCTGCTGACCTGACCACTGATGATGATGATGATGATGATGATGATGATGATG 893
 Qy 601 ATTTTGACGCAACTACTTCTGCTCCCTCCCTGCTGATGATGATGATGATGATGATGATG 660
 Db 894 ATTTTGACGCAACTACTTCTGCTCCCTCCCTGCTGATGATGATGATGATGATGATGATG 953
 Qy 661 ATTTTGACGCAACTACTTCTGCTCCCTCCCTGCTGATGATGATGATGATGATGATGATG 720
 Db 954 ATTTTGACGCAACTACTTCTGCTCCCTCCCTGCTGATGATGATGATGATGATGATGATG 1013
 Qy 721 AGGCTAACCATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 780
 Db 1014 AGGCTAACCATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 1073
 Qy 781 AGGCTAACCATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 840
 Db 1074 AGGCTAACCATTTCTCTACTCTTGTGATTTTACGATGTTTATACCTTCCATATCTTG 1133
 Qy 841 CATGAAGCTTACATGCTTCTAGACCATTAAGTCTGTCTGACACCTTTGGTAACTCTTGA 900
 Db 1134 CATGAAGCTTACATGCTTCTAGACCATTAAGTCTGTCTGACACCTTTGGTAACTCTTGA 1193
 Qy 901 CTATATGTTGTTGCTGACGACCAACTTTCAGACGCTGTCTGCTCAACAGTGAAGTCAAA 960

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Db | 1194 CTATATGTGTGTGTCACGACACTTTCAGCGCTGTCTCTCAACAGTGAGATGCAA 1253
QY 961 GTAGCGGGAACCTTGAGCAAGCAAGAAATTAAGTTACTCAACCAACCTTGA 1014
Db 1254 GTAGCGGGAACCTTGAGCAAGCAAGAAATTAAGTTACTCAACCAACCTTGA 1307

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